Tue May

CE GPCR19,2

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

8, 2006, 09:27:07; Search time 231 Seconds (without alignments) 1212.531 Million cell updates/sec May Run on:

US-10-650-467-105 2074 Title: Perfect score:

1 MVSSAATISTISTITTPSTI.....QLHDLLPTSTHSDRCAGNSF 397 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 Total number of hits satisfying chosen parameters:

2166443 seqs, 705528306 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q90415 caenorhabdi Q6f3c9 caenorhabdi Q2527 caenorhabdi Q2305 caenorhabdi Q290475 drosophila Q629b2 caenorhabdi Q629b2 caenorhabdi Q1q0b9 anophales g Q61048 caenorhabdi Q1014 caenorhabdi Q81014 caenorhabdi Q20275 caenorhabdi Q61144 caenorhabdi Q60114 caenorhabdi Q60114 caenorhabdi Q60114 caenorhabdi Q60118 caenorhabdi Q60118 caenorhabdi Q60119 caenorhabdi Q6011 caenorhabdi Q60118 drosophila Q60118 caenorhabdi Q60118 caenorhabdi Q60118 caenorhabdi
SUMMARIES	067315 067327 CAEEL 065227 CAEEL 0233105 CAEEL 0233105 CAEEL 020825 CAEEL 052062 CAEEL 070089 ANOGA 01833 CAEEL 010104 CAEEL 090004 CAEEL 090004 CAEEL 091014 CAEEL 091014 CAEEL 020275 CAEEL 020275 CAEEL 020275 CAEEL 020275 CAEEL 020276 CAEEL 020276 CAEEL 020276 CAEEL 020276 CAEEL 020277 CAEER 050481 DEGEL 050481 CHIMAN 050209 HUMAN 050209 HUMAN 060481 CHICK 061871 CAEER 061871
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Length	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
\$ Query Match	20010000000000000000000000000000000000
Score	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
Result No.	1 1 2 2 4 4 3 3 2 5 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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GPRIO_RAT Q9YHXI_GADMO Q700NY_ANGGA Q5CGMS_ANGGA Q4SRZ3_TETNG G50115_FUGRU G59115_FUGRU G99N324_CAREL Q61SK7_CAREL Q61SK7_CAREL Q61SK7_CAREL Q61SK7_BRAIT Q6PR57_BRARE Q50111_FUGRU
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ALIGNMENTS

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Threstigating biology.";

RI SCIENCE SPACETION TOTATION: Integral membrane protein (By similarity).

RI SCIENCE SPECTION TOTATION: Integral membrane protein (By similarity).

BE EMBL; ACOGGOS; ARFGOSIS.3; -; Genomic DNA.

BE EMBL; ACOGGOS; ARFGOSIS.3; -; Genomic DNA.

BE NOTHBASE; WESCHOOLOSISS; YSGGSA.4.

BY NOTHBASE; WESCHOOLOSISS; YSGGSA.4.

BY NOTHBASE; WESCHOOLOSISS; PECCEPTOR TOTATION: IEA.

BY GO; GO:00016021; Cintegral to membrane; IEA.

GO; GO:00016021; Cintegral to membrane; IEA.

GO; GO:000186; P: rhodopsin-like receptor activity; IEA.

GO; GO:000186; P: G-protein coupled receptor protein signalin. .; IEA.

GO; GO:000186; P: Signal transduction; IEA.

BY GO; GO:0001165; P: Signal transduction; IEA.

GO; GO:0001165; P: GPRCRENODOPSN.

BY FRONTE; PRO10237; GPCRRHODOPSN.

BY FRONTE; PRO10237; GPCRRHODOPSN.

BY ROSTE; PSSOGS2; G PROTEIN RECEP PI 2; 1.

KW Complete proteome; G-protein coupled receptor; Hypothetical protein;

KW Complete proteome; G-protein coupled receptor; Transmembrane.

SEQUENCE 397 AA; 44536 MW; 092ER3CAGAFFSER CRC64;
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                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
MEDLINE=90605613; PubMed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                     397 AA.
                     PRT;
OBVARS CAREL PRELIMINARY;

09N4RS;

01-OCT-2000 (TrEMBLrel. 15, Cx

01-JUN-2003 (TrEMBLrel. 24, La

01-OCT-2003 (TrEMBLrel. 25, La

Hypothetical protein.
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                 SWWW RREPRESENT TO THE PROPERTY OF THE PROPERT
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TTVMILGEVVEMAVITYCYFKILGKVSKDMIIGNAGFCGGILGKQRSDATSRKKKVNYIL 288
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                                                                                                                                      241 AVITYCYFKILQKVSKDMILQNAQFCQSLIQKQRSDATSRKKKVNYILIAMVVTFIGCML 300
                                                                                                                                                                                                                                                TVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTA 108
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                                                                                                       241 AVITYCYFKILQKVSKDMIIQNAQFCQSLIQKQRSDATSRKKKVNYILIAMVVTFIGCWL
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STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6238;
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SROUENCE 444 AA; 50089 MM; B1794980E7DFC16A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.3%; Score 1768.5; DB 2
91.0%; Pred. No. 5.7e-126;
ive 11; Mismatches 10;
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Matches 342; Conservative
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Q62527;
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NUCLEOTIDE SEQUENCE.
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                                                                241 AVITYCYFKILQKVSKDMIIQNAQPCQSLTQKQRSDATSRKKVNYILIAMVVTFIGCWL 300
                                                                                                                                                                                                                                                   PLTLLNLVKDFKKEPEWLKROPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRSGLSKIL 360
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Science 28:2012-2018(1998).

C. -1. SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

RMBL, ACO06808; AAT68899.;

RMBL, ACO06808; AAT68899.;

R MormBase; WBGene00021983; YS6G8A.4.

R WormBase; WBGene00021983; YS6G8A.4.

R O; GO:0016021; Cintegral to membrane; IRA.

RO; GO:001881; P:rhodopsin-like receptor activity; IRA.

RO; GO:001887; P:rhodopsin-like receptor activity; IRA.

RO; GO:001186; P:d-protein coupled receptor protein signalin. .; IRA.

RO; GO:0007165; P:signal transduction; IRA.
                                    STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM
                                                                                                                                         AVITYCYFKILQKVSKDMIIQNAQPCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGGWL
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Complete proteome; G-protein coupled receptor; Hypothetical protein;
Receptor; Transducer; Transmembrane.
SEQUENCE 433 AA; 46819 MM; 57D033P5FDDA70P5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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91.6%; Score 1899; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.8e-136;
Matches 364; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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MEDLINE-99069613; PubMed-9851916;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
Hypothetical protein.
ORFNames=158G8A.4;
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Name=NPFR76F; ORFNames=CG7395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                Q9VW75 DROMB PRELIMINARY;
Q9VW75; Q9VW74;
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C. 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL: Z38067; CAB01528.2; -; Genomic_DNA.
BRHS: T27559; T27559.
RRHS: T27559; T27559.
RRHS: T27559; T27559.
RRHS: T27559; T27559.
ROMEBase: WEGENERORISB3; ZC412.1;
ROMEBase: WEGENERORISB3; ZC412.1.
ROMEBASE: WEGENERORISB3; ZC412.1.
ROMEBASE: RECEPTOR TEACHILY; IEA.
GO: GO:00016021; C:integral to membrane; IEA.
GO: GO:00016021; C:integral to membrane; IEA.
GO: GO:0001827; F:receptor activity; IEA.
GO: GO:000186; P:rhodopsin-like receptor activity; IEA.
GO: GO:000186; P:rhodopsin-like receptor protein signalin. .; IEA.
RO: GO:0007165; P:signal transduction; IEA.
RITHERPO: IPRO00261; NPY receptor.
RITHERPO: IPRO00611; NPY receptor.
REPERO: PRO00011; Tem_1; 1.
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  IAMVVTFIGCWLPLTLLNLVKDFKKRPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT 348
                     93 FLINLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 RYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYPL------YYSQNLKTWVIENV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 PYCGHFCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265
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PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
Complete proteome; G-protein coupled receptor; Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.3%; Pred. No. 8.5e-38; ive 76; Mismatches 111; Indels
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                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypotherical protein ZC412.1.
ORFNames=ZC412.1;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
MEDLINE=99069613; Pubmed=9851916;
                                                                                                               349 RKOKRSGLSKILNSTE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                   Q23305_CAEEL PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Bristol
  289
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Goard. 3.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocay. 3.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Bardon R.C., Roges Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.W., Bard A., Baxendala J., Baytaktaroglu L., Beasley B.M.,

RA Beson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolahakov S.,

RA Burtis R.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Perract C., Perriact S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.B., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.B., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Mouse M., Helmander J.R., Thoeyam C.,

RA Goler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Goler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Classer K.,

RA Goler C., Gabrielian A.E., Karaft C., Kravitz S., Kulp D., Lai Z.,

RA Golek A., Gong F., Gorrell J.H., Wei M.-H., Ibegwan C.,

RA Harris N.L., Harvey D.A., Heimand T.J., Wei M.-H., Ibegwan C.,

RA Liu X., Matterl B., Wollroad T.C., McLeod M.-P., Moshreii A.,

RA Liu X., Matterl B., Wollroad T.C., Mcraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Matterl B., Wollroad T.C., Mcraft C., Kravitz S., Kulp D., Lai Z.,

RA Blazzolo M. Pittenna G.S., Pan S., Pollard J., Murry W. Secleel F. F.,

Reiner K., Remington K., Saunders R.D.C., Scheeler F., Ren R.,

RA Shriekas R., Tector C., Thurer R., Wang A., Wallshiam S.M., Woolly G., Shen B., Wang S., Yung S., Zhan M., Rang S., Waller S., Sheeler E., Shen S., Wang S., Waller S.,
                                                       236 ---LTAAQQAQTAVRKRRVMYVLJIMVIVFMACWFPLSAVNLFRDLGMRFEFCQTVYKVL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22426065; PubMed=12537568;
Celniker S.B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
266 COSLIQKORSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKBPEW--
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 10-MAY-2005 (TrEMBLrel. 30, Last annotation update) CG7395-PA (GH23382p) (Neuropeptide F-like receptor)
                                                                                                                                                                                                                                      293 MADQMYFKLLNVHVIAMTSIVWNPVIYFWMSKRHRRA 329
                                                                                                                                                                               318 LKROPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRS 354
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

C. -| SUBCELLULAR LOCATION: Integral membrane protein (By similarity). REMBL, AR003514; AAR49074.2; -; Genomic_DNA.

REMBL, AV051588; AAR49045.1; -; MRNA.

REMBL, AV192578; AAR9465.1; -; mRNA.

REMBL; AV192579; AR099461.1; -; mRNA.

RINBAGE; FBGN0036934; MPRR76F.

RINBAGE; FBGN0036934; MPRR76F.

ROJ GO:0008188; Fineuropeptide receptor activity; IDA.

RINEAPO; IRRO00276; GBCR_AR0498...

RINEAPO; IRRO00511; NPY_receptor.
                                                                                      [3]
NUCLECTIDE SEQUENCE.
NUCLECTIDE SEQUENCE.
NUCLECTIDE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminter J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Whon G.M., Celniker S.,
submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berkeley Drosophila Genome Project, Celniker B., Frise E., George R. Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R. Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith I Yu C., Rubin G., Rubin G., Brand B., Swith I "Brosophila melanogaster release 4 sequence.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0237; GPCRRHODOPSN.
PRINTS; PRO1012; NRPRETIDEYR.
PROSITE; PS01237; G-PROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Neuropeptide; Receptor; Transducer;
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgum: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66579 MW; EEG3BEF821BDA14B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase;
Submitted (MAR-2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
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SEQUENCE 60
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Length 600;

DB 2;

25.5%; Score 529;

Query Match

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247 YPKILQKVSKDMIIQNAQPCQSLTQKQRSDA-TSRKKKVNYILLIAMVVTFIGCWLPLTLL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                              306 NLVKDF-KKRPEWLKRQPFFWAINAHVIAMSLVVWNPLLPFWLT---RKQKRSGL---- 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The C.briggsae Sequencing Consortium;
The C.briggsae Sequencing Consortium;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; CARCO110000002; CARS7235.1; -; Genomic DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004887; F:receptor activity; IEA.
GO; GO:0001884; F:receptor activity; IEA.
GO; GO:000186; P:rhodopsin-like receptor activity; IEA.
GO; GO:0001165; P:signal transduction; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000611; NPY_receptor.
InterPro; IPR000611; NPY_receptor.
                 12;
                                                                                                                                                                                                                                                                                                                                               ------ETPYCGHPCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                                                                                                                                                                                                                                                                                                                                                                      242 TSATQAYMQVMTAGSTGPEMPYVRVYCEB-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
                                                                                                                                                62 VQIFFYVLYATVEVIGVEGNVLVCYVVLRNRAMQTVTNIFITNLALGBILLCVLAVPFTP 121
                                                                                                                                                                                                                         122 LYTFWGRWAPGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRWKLSTCIGI 181
                                                                                                                                                                                                                                                                        174 TFLIWIVSTLINLPYLMSFE---- 204
                                                     23
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                                                   6 ATISTISTITIPST-----ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY
                                                                              2 ANLSWLSTITTTSSSISTSQLPLVSTTNWŠLTSPGTTSALLADVAASDEDRSGGIIHNQP
                                                                                                                         54 IRSIFTFLYGFLYVLGIFGNGGVLMAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP
                                                                                                                                                                                                  114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                   80; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1. G-protein coupled receptor; Hypothetical protein; Receptor; Transducer; Transmembrane.
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42616 MW; 341E2844A0156E9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
30.5%; Pred. NO. 1.1.
tive 76; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SKILNSTEGSKKAGGSGLRGIQLH 380
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01012; NRPEPTIDEYR.
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Q62982;
                        Matches 136; Conservative
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375 AA;
     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004
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NON TER
SEQUENCE
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                                                                                                           KIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSD----- 276
                                                                                                                                                                                                     SIROALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANW-QSENSR 224
                                                                                                                                                                                                                                        ----ATSRKKKVNYILIAMVVTFIGCWLPLTLINLVKDFKKEPEWLKRQPFFWAINAHVI 332
                                                                                                                                                                                                                                                     242 QQRMAVKRRQKTNRMLIGMVVAPACSWIWSVTFNILRDYBYLPDLIKNQEYIFGIATHCI 301
                                                                46 DDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILV
                            Gaps
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PROSITE, PS50263; G PROTEIN RECEP F1 2; 1.
Complete proteome; G-protein coupled receptor; Hypothetical protein;
Receptor; Transducer; Transmembrane.
SEQUENCE 468 AA; 52773 MW; 2A0F72C78EE353D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                            45;
   Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MDELINE-29065613; PubMed-2851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
25.0%; Score 518.5; DB 2; Length 33.3%; Pred. No. 4.1e-31; ive 68; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                     AMSLVVWNPLLFF------WLTRKOKRSG 355
                                                                                                                                                                                                                                                                                                    302 AMTSIVWNPLLYAVLNLQLRAAFIDLMPQWLRRRLNLDG 340
                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypotherial protein C16D6.2.
ORFNames=C16D6.2;
Caenorhabditis elegans.
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PRINTS; PR01012; NRPEPTIDEYR.
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                        Matches 113; Conservative
Query Match
Best Local Similarity
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148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EWLKROPFFWAINAHVIAMSLVVWNPLLF-------FWLTRKOKRSG--LS 357
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121 ISIDRYILIRFPMRKPITHYQAVGVIAIICAFAATITSPIM--FKQKLGEF----ENF
                                                                                                                                                                                                                                                     89 ARNVFLLNLIFTDLILVFTAIPVTPWYAMTKOWAFGSVMCHLVPLSNSCSVFVTSWSLTA
                                                                                                                                                                     29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukāryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Anopheles gambiae Sequence Committee;

Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

-I-CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AAAB01008986; EAA40213.1; -; Genomic_DNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:rhodopshi-like receptor activity; IEA.

GO; GO:0001584; F:rhodopshi-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. .;

R GO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR000276; GPCR_Rhodpsn.

R InterPro; IPR000276; GPCR_Rhodpsn.
                                                                               48;
                        Length 468;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                            74; Mismatches 128;
11arity 31.3%; Pred. No. 1.1e-30; Conservative 74; Mismatches 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=GPRNPY3; ORFNames=ENSANGG00000009317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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PRINTS; PR01012; NRPEPTIDEYR.
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01-MAR-2004 (TrEMBLrel. 26, 1
01-MAR-2004 (TrEMBLrel. 26, 1
ENSANGP00000011806 (Fragment)
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Q7Q0B9;
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                                                 Similarity
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               Query Match
Best Local Simil
Matches 114; C
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NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 LIFFI --AHLTAMSSTCYNPFLYAMLNDNFRKEPKQVLPCFDPSRGRAGTVGGNRGAGGG 417
                                                                                                                                                                                                                                                                                                                                                                                    93 FILINLIPTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 KFLHINDPTKOPVSIRQALAITFLIWIVSTLINLPY------LMSFEHVDGSFYVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 -SSAMYC-----BELWPSEEMRKTFSIVTSILQFVLPFIIMAPCYICVSIRLANDRARTKP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 AQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKE-PEWLKRQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 PFFWAINAHVIAMSLVVWNPLLFFWLT----RKQKRSGL-----SKILNSTEGSKKAGGSG 373
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor I family.
EMBL; CAACO1000068; CAE68647.1; -; Genomic DNA.
GO, GO:0010621; Cintegral to membrane; IEA.
GO; GO:0001893; F:neuropeptide X receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:s-procein coupled receptor protein signalin. .; IEA.
GO; GO:0007165; P:s-grani transduction; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                         5 AATISTISTITTPSTISNVITSHSN-----52
                                                                                                                                                                                                                                                                                14 AVTVAT-ATSTSPAAMASLVLDHTELPLAGTIPPAALMPARVLLPSNATNLTLTLBELLR 72
                                                                                                                                                                                                                                                                                                                                                     53 ------YIRSIPTPLYGPLFVLGIFGNGGVLWAVARNKRLQSARNV 92
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transducer; Transmembrane.
NON_TER 470 470
                                                                                                                                                                                                        81;
                                                                                                                                                     Query Match 23.9%; Score 495.5; DB 2; Length Best Local Similarity 27.3%; Pred. No. 2.9e-29; Matches 121; Conservative 84; Mismatches 158; Indels
                                                                                                         470 AA; 51957 MW; B99EBDE9B505DC4D CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 AA
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Name=CBG14540;
Caenorhabditis briggsae.
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PRINTS; PR00237; GPCRRHODOPSN
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061808;
25-OCT-2004 (TYEMBLYEL 26
25-OCT-2004 (TYEMBLYEL) 28
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                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                    29 FLCVYIFLFFIGLFGUVTLIYVTCSYKALLSVQNIFILMLAASDIMMCILSLPITFITNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYCOMAPGSVMCHLVPLSNSCSVPVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 OKORSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKBPEWLKRQPFF----
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EMBL; U49944; AAA93419.1; -; Genomic_DNA.

PIR; T29741, T29741.

WormBase; WBGene00003807; npr-1.

WormBase; WBGene00003807; npr-1.

WormPep; C3986.6; C2065941.

G0; G0:0016021; C:integral to membrane; IEA.

G0; G0:0004872; F:receptor activity; IEA.

G0; G0:0001584; F:rhodopsin-like receptor activity; IEA.

G0; G0:0001584; P:rhodopsin-like receptor activity; IEA.

G0; G0:0001584; P:rhodopsin-like receptor activity; IEA.

G0; G0:000158; P:receptor activity; IEA.

G0; G0:000158; P:receptor activity; IEA.

G0; G0:000158; P:receptor activity; IEA.
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                            Gabs
                                                                                                                                                                                                                                                                         77;
                                                                                                                                                                                                              Length 453;
PRINTS; PRO1012; NRPEPTIDEYR.

PROSITE; P600237; G PROTEIN RECEP F1 1; 1.

G-protein coupled receptor; Hypothetical protein; Receptor; Transducer; Transducer; Transembrane.

SEQUENCE 453 AA; 52101 MW; 38A7P401B1054A3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Neuropeptide receptor family protein 1.
                                                                                                                                                                                                           Query Match 23.5%; Score 487.5; DB 2; Best Local Similarity 30.5%; Pred. No. 1.1e-28; Matches 118; Conservative 77; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 QKMLNBAKNSNGRMKNGNSCLKERELN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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MEDLINE-99069613; PubMed-9851916;
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Science 282:2012-2018(1998).
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Q18534;
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Q9xxu4_CAEEL PRELIMINARY;
Q9xxu4;
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                                                                                                                                                                                                                                                                                                                                                                                                                             118 TKOWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLI 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYDISYLLNLFTHSIAMSNNVLNPVLYAMLNPSFRQLVIKTYFGDRRKSDRIINQTSVYK 375
                                                                                                                                                                                                                                                                                                                                                                  pfam; pp00001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODOPSN.
PROSITE; PS00237; G-PROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00237; G-PROTEIN RECEP_F1_1; UNKNOWN_1.
COMPLETE; PSS0262; G-PROTEIN RECEP_F1_2; 1.
Transducer; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFV
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                                                                                                                                                                                                                                                                                                   Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
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Science 282:2012-2018 (1998).
-- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL; Z68216; CAD59147.1; -; Genomic_DNA.
EMBL; Z68219; CAD59147.1; -; Genomic_DNA.
EMBL; Z68216; CAD59157.1; JOINED; Genomic_DNA.
EMBL; Z68216; CAD59155.1; JOINED; Genomic_DNA.
ENGL; Z68216; CAD59156.1; Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                77;
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                                                                                                                                                                                                                                                    23.4%; Score 485.5; DB 2; Length
                                                                                                                                                                                                                                                                                            69; Mismatches 117; Indels
                                                                                                                                                                                                     457 AA; 52464 MW; 6EB950A91BB10BE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein npr-2.
Name-npr-2; ORPMames=705A1.1, T05A1.1a;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                         Pred. No. 1.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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InterPro; IPR000276; GPCR_Rhodpsn
InterPro; IPR000611; NPY_receptor
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MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                         30.8%;
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Matches 117; Conservative
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QBIOL4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 LIQLHSS--QMINETEETCDRYIDKHPDMTNEPTVLVTFSLLYLHIFLLGILGNSAVLYL 93
CONTROL OF CLINEGES TO MEMBRANDS IEA.

CO:0016021; C:integral to membrane; IEA.

RO; GO:0004983; F:neuropeptide Y receptor activity; IEA.

RO; GO:0004983; F:neuropeptide Y receptor activity; IEA.

RO; GO:000184; F:rhodopsin-like receptor activity; IEA.

RO; GO:000186; F:d-protein coupled receptor protein signalin. ..; IEA.

RO; GO:0007186; F:signal transduction; IEA.

InterPro; IPR0000276; GPCR_Rhodopsn.

InterPro; IPR00001; 7tm 1; 1.

RINTS; PR00137; GPCRHODOPSN.

RRINTS; PR00137; GPCRHODOPSN.

RRINTS; PR0137; GPCRHODOPSN.

RRINTS; PR01012; NBPETIDEYR.

RRINTS; PR01012; NBPETIDEYR.

RRINTS; PR01012; NBPETIDEYR.

RRINTS; PR01012; RECEP_F1_1; 1.

RR PR05ITE; PS00237; G PROTEIN RECEP_F1_2; 1.

COMPLETE protein Coupled receptor; Hypothetical protein;

R Receptor; Transducer; Transducer; Transducer;

SEQUENCE 430 AA; 49138 MW; 480E88990C94CB9E2 CRC64;
                                                                                                                                                                  IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 TWKHRQLQTVQNIFILNLCASNVLMCLTSLPITFITNVYKQWFFSSPVCKLIPLVQGASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 VITSHSNNGSCIQIAEAIAAQGID -- - DITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LCGSYCSE-HWPLAEVRKGYTFLVLITQFLFPFATMAFCYYNIFSRLRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 ----LOKVS-KDMIIQNAQFC------QSLTQKQRSDATSRKKKVNYILIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 VARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 FVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPY--LMSFEHVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 SFYVQPGETPYCGHFCDBANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKI----
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2004 (TrEMBLrel. 25, Last annotation update)
01-NAR-2004 (TrEMBLrel. 25, Last annotation update)
0RFNames=C53C7.1, C53C7.1a.
Caenorabditis elegans.
Elbaryota; Metazca; Nemtoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 430;
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The C. elegans sequencing consortium;
Genome sequence of the nematode C. elegans: a platform for investigating biology.";
Science 282:2012-2018 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 22.3%; Score 462; DB 2; Length 430 Best Local Similarity 28.4%; Pred. No. 9.1e-27; Matches 112; Conservative 83; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 MVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 SLVVWNPLLFFWLTRKQKRSGLSKILNSTEGSKKA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 LTNVTNPFLYAWINPMFKEMLIKTLRGGSKSPKPA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] TOCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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the nematode C. elegans: a platform for
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Q22188;
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   sequence of
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Matches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVRNMPIVSLSVSDIFVAIVSGSVTPITAFSKVWLFGGFLCHLLPLLGGTALSFSTLTLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AISLDKFLHINDFTKQPVSIRQALAITFLIWIVSTLINLPY----LMSFEHVDGSFYVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 PGETPYCCHPCDEANWQSE-NSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 NAQPCQSLTQKQRSDATSRKKKVNYILLIAMVVTPIGCWLPLTLLNLVKOFKKRPEWLKRQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 GSQ--KELMSEARRQLIQRRLRINRMLIIMIVTPALSWLPSVGFNFLRDYSALFGIIDSQ 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00237; GFCRHODOPSN.
PRINTS; PR01012; NRPETIDEYR.
PROSITE; PS00237; G PROTEIN EXCEP_F1_1; UNKNOWN_1.
PROSITE; PS0262; G PROTEIN RECEP_F1_2; 1.
Complete protecome; G-protein coupled receptor; Hypothetical protein;
O44820:F52C6.3; NDExp=1; IntAct=EBI-318084, EBI-318098;
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL: ALOOBEG8; CAAISS13.1; -; Genomic_DNA.
PIR; T2O.184; T2O.184.
HSSP; P02699; 1L9H.
                                                                                                                                                                                                                                                      WormPep; C5377.1a; CE19767.

GO; GO:0016021; C:integral to membrane; IBA.

GO; GO:0004983; P:neuropeptide Y receptor activity; IEA.

GO; GO:0004189; P:receptor activity; IBA.

GO; GO:0001189; P:receptor activity; IBA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR000276; GPCR Rhodpan.

InterPro; IPR000271; NPY receptor.

Pfam; PF00001; 7tm 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.3%; Score 461.5; DB 2; Length 30.9%; Pred. No. 8.4e-27; Live 79; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transducer; Transmembrane.
SEQUENCE 365 AA; 40860 MW; 5DB21F7EBF5B99AF CRC64;
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25-0CT-2004 (TYEMBLrel. 28, Last sequence update)
25-0CT-2004 (TYEMBLrel. 28, Last annotation update)
Hypothetical protein C3277.1b.
ORFNames=C33C7.1, C53C7.1B;
Caenorhabditis elegans.
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STRAIN=Brise() N2;
MEDLINE=B0069613; PubMed=9851916;
The C. elegans sequencing consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
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                                                                                                                                                                                                Ensembl, C53C7.1, Caenorhabditis elegans.
                                                                                                                                                                                                                                      WormBase; WBGene00008278; C53C7.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 30.34 Matches 110; Conservative
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SARNVFLLNLIPTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLT 147
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                                                                                                                                                                          WormPep; C53C7.1b; CE36989.

GO; GO:0016021; C:integral to membrane; IRA.

GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.

GO; GO:0004892; F:receptor activity; IRA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IRA.

GO; GO:0001786; F:G-profein coupled receptor protein signalin. ..; IEA.

InterPro; IPR000276; GPCR_Rhodopsu.

InterPro; IPR000216; GPCR_Rhodopsu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SVRNMFIVSLSVSDIFVAIVSGSVTPITAFSKVWLFGGPLCHLLPLLQGTALSFSTLTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 PGETPYCGHPCDEANWQSE-NSRKIYGTTVWLLQFVVPMAVITYCYFKILQKVSKDMIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 NAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLINLVKDFKKEPEWLKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 SNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00037; GPCRRHODOPSN.
PRINTS; PR01037; GPCRRHODOPSN.
PRINTS; PR01012; NRPEPTIDETR.
PROSITE; P800137; GPCRTEIN ERCEP_F1 1; UNKNOWN 1.
COMPLETE PS00262; G PROTEIN ERCEP_F1 2; 1.
Complete proteome; G-protein coupled receptor; Hypothetical protein;
Receptor; Transducer; Transmembrane.
SRQUENCE 362 AA; 40577 MW; D81B10D5CF877651 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                    protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPFWAINAHVIAMSLVVWNPLLFFWLTRKOKRSGLSKILNSTEGS 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.2%; Score 461; DB 2; Length 36 31.3%; Pred. No. 9.1e-27; Live 77; Mismatches 136; Indels
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01-NAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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investigating biology.";
Science 282:2012-2018(1998).
-!- SUBCELLULAR LOCATION: Integral membrane premb; ALO08868; CAH04724.1; -; Genomic_DNA. Ensemb], C53C7.1; Caenorhabditis elegans.
WormBase; WBGene0008278; C53C7.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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SEQUENCE [LARGE SCALE GENOMIC DNA]

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it investigating biology.";

L. Science 282:2012-2018(1998).

C. SubezeLiular Lockation: Integral membrane protein (By similarity).

C. SubezeLiular Lockation: Integral membrane protein (By similarity).

C. SubezeLiular Lockation: Othe G-protein coupled receptor 1 family.

B. FIRE, 724487. 724487.

R. FIRE, 724487. 724487.

R. Ensembl; 70541.1; Caenorhabditis elegans.

R. MormBase; WBGaneo0003808; npr-2.

R. WormPep; 70541.1b; CE32925.

R. WormPep; 70541.1b; CE32925.

R. GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0004893; F:neuropeptide Y receptor activity; IEA.

GO; GO:0004893; F:neceptor activity; IEA.

GO; GO:0001864; F:neceptor activity; IEA.

GO; GO:0007165; P:G-protein coupled receptor protein signalin. .; IEA.

GO; GO:0007165; P:gignal transduction; IEA.

RO; GO:0007165; P:gignal transduction; IEA.

InterPro; IPR000261; NPY_receptor.

R. InterPro; IPR00011; NPY_receptor.

R. Fam: PP00001: 7rm 1: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVS 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---DGFFFHSDETSATSTDHTYIVSMTAHLISMLINVINPFLYAWLNPMFKEMLIKTLRG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IROALAITFLIWIVSTLINLPY--LMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIYGTTVMLLQFVVPMAVITYCYFKI------LQKVS-KDMIIQNAQFC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 VSINAEAVQNGLENKQRLAVLAQQRRTTTILSCMVLLPAFTWLPHNVVTLMIEY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 LKRQPFFW-------AINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKILN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDPKKEPEW
                                                                                                                                                                                                                                                                                                                                                                                                                    65; Gaps
                                                                                                                                                                                                                                                                                             PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Complete proteome; G-protein coupled receptor; Hypothetical protein;
Receptor; Transducer; Transmembrane.
SEQUENCE 387 AA; 44128 MW; 195C02A8A65772FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 22, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAPpothetical protein F41E7.3.
02enorhabditis elegans.
02enorhabditis elegans.
03enorhabditis elegans.
04enorhabditidae; Peloderinae; Caenorhabditis.
05enorhabditidae; Peloderinae; Caenorhabditis.
07el_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                      22.2%; Score 460.5; DB 2; Length 387; 28.5%; Pred. No. 1.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                   80; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                           387 AA; 44128 MW; 195C02A8A65772FE CRC64;
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PRINTS; PR01012; NRPEPTIDEYR.
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Q20275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 STEGSKKA 369
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Matches 105; Conserv
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67 VLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSV 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 WIVSTLINLPYL----MSPEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVML 233
                                                                                                                                     Threstigating biology.";

Investigating biology.";

Science 282:2012-2018(1998).

C. -- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

C. -- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

C. -- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

D. REAL, Z68106; CAA92126.2; -; Genomic_DNA.

RESEMBL; Z68106; CAA92126.2; -; Genomic_DNA.

RESEMBL; F41E7.3; CG1509.

R. WOTHBEAS; WBGeneCO009619; F41E7.3.

RO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:000188; P:receptor activity; IEA.

GO; GO:000188; P:receptor activity; IEA.

GO; GO:000186; P:signal transduction; IEA.

GO; GO:000186; P:signal transduction; IEA.

InterPro; IPRO00611; NPY_receptor.

InterPro; IPRO00611; NPY_receptor.

InterPro; IPRO00613; TAM 1; 1.

DR PRINTS; PRO0137; GPCRRHODOPSN.

PRINTS; PRO0137; GPCRRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . ., IEA.
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PROSITE; PS50262; G_RROTEIN_RECEP_F1_2; 1.
PROSITE; PS00626; RCC1_2; UNKNOWN 1.—
Complete protecome; G-protein coupled receptor; Hypothetical protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 IFAICWFPFNLLNCLRDLKLD-NFWRGYFSFVFLSVHLMSMTATAMNPILYAFM 314
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                                                                                                                elegans: a platform for
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                                                                               The C. elegans sequencing consortium, "Genome sequence of the nematode C. e
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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BD234417 DNA encod
AR634065 Sequence
CS064391 Sequence
AX840908 Sequence
AX840908 Sequence
AF257210 Homo sapi
BD165901 7TM recepto
BD217139 HOWY Y7 re
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AX75083 Sequence
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AF309091 Gallus ga
X57764 Rat mRNA fo
B03623 DNA encodin
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1 (bases 1 to 1193)

Lowery, D.E., Geary, T.G., Kubiak, T.M. and Larsen, M.J.

G protein-coupled receptor-like receptors and modulators thereof
Patent: 108 6632621-A 104 14-OCT-2003;
Pharmacia & Upjohn Company; Kalamazoo, MI
                                                           S65355 nonselectiv
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AR408593
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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                                       E03623
S65355
AF268899
AF330053
                                                                                                               BD234417
AR489066
CS064391
AX840908
AP257210
AP257210
AP257210
AP256031
BD165911
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AP2663113
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/organism="unknown"
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Best Local Similarity 100.
Matches 1193; Conservative
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AC006705 Caenorhab
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                 GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Result Š. Euteleostomi;

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             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelec
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

    >>1191
/note="unnamed protein product; Clone identifier:

                                                                        Lowery, D.E., Geary, T.G., Kubiak, T.M. and Larsen, M.J.
G protein-coupled receptor-like receptors and modulators
Patent: WO 0138533-A 104 31-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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ACCAAACAACCAGITTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGAAGCTTTTAC

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PAT 22-JUN-2001

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AX151319 1193 bp 1 Sequence 104 from Patent W00138533. AX151319 AX151319.1 GI:14533456

LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 2 AX151319

Homo sapiens (human)

541

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ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC

480 786 540 846 9 906 9 996 720

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PAT 18-DEC-2003
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Lowery, D.B., Geary, T.G., Kubiak, T.M. and Larsen, M.J.
Gary, T.G., Kubiak, T.M. and Larsen, M.J.
Gary, D.B., Geary, T.G., Kubiak, T.M. and modulators thereof
Patent: US 6632621-A 106 14-0CT-2003;
Pharmacia & Upjohn Company; Kalamazoo, MI
                                                                                                                                                                                                                                                    1207 CCTTTAACATTACTCCAATTTGGTCAAAGAGTTTTTAAAAAAGAGCCCGAATGGCTAAAAAGG
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                727 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC
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GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC
                                                        ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC
                                                                                                                 541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC
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Sequence 106 from patent US 6632621.
AR408594

    1301
    /organism="unknown"
    /mol_type="genomic DNA"

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                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                       Lowery, D.E., Geary, T.G., Kubiak, T.M. and Larsen, M.J. G protein-coupled receptor-like receptors and modulators thereof Patent: WO 0138533-A 39 31-MAY-2001; PHARMACIA & UPODIN COMPANY (US)
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0;
                                                            linear
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    1500
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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39 from Patent WO0138533.
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                                                                                                                                    Homo sapiens (human)
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                              RESULT 4
AX151254
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Query Match	Qy 241 GCGAGAAACAAGGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300 Db 241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCCACTTGATCTTCACC 300 Call ACCAAACAACAAGCGCTCCAATCGGCTACTTTCTGCTCAACTTGATCTTCACC 300 Call ACCAAACAACAACAACTTCACTACCACCATGGTACGCATGACCAAACAACAACAATTCACTTTCTCTTGTCAACTTCACTTTCACTTTCTTT		

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Submitted (23-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                   ACUOE808 34544 bp DNA linear INV 23-JUN-2005
Caenorhabditis elegans cosmid Y58G8A, complete sequence.
AC006808
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Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-2002) Department of Genetics, Washington
Genome Sequencing Center, 4444 Forest Park Avenue,
1110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-NOV-2001) Department of Genetics, Mashington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (07-UNM-2002) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
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4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
5. (bases 1 to 34544)
Waterston,R.
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Submitted (24-JAN-2003) Department of Genetics, Washington
                                                                                                                                                                                                                                                                                                                                 C. elegans Sequencing Consortium
Genome sequence of the nematode C. elegans: a platform for
investigating biology
Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                            Caenorhabditis elegans
Caenorhabditis elegans
Bukaryota; Metazos; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University, 4444 Forest Park Avenue, St. Louis, S. (bases 1 to 34544)
                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 34544)
Tin-Wollam,A., Graves,T. and Harrison,M.
The sequence of C. elegans cosmid Y58G8A
Unpublished (2001)
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Louis, MO 63110, USA
8 (bases 1 to 34544)
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Submitted (28-MAR-2000)
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10 (bases 1 to 34544)
                                                                                                                                                                                                                                                                                                  (bases 1 to 34544)
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Waterston, R.H.
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Direct Submission
Submitted (08-JUL-2004) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
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Submitted (22-SEP-2004) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUN-2005) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
      St.
  Genome Sequencing Center, 4444 Forest Park Avenue,
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Department of Genetics, Washington University
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
                   Louis, MO 63110, USA
11 (bases 1 to 34544)
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13 (bases 1 to 34544)
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                                                          Wilson, R.
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TICE: This sequence may not be the entire insert of this clone. may be shorter because we only sequence overlapping sections e. or longer because we provide a small overlap between neighboring submissions.

email: submissions@watson.wustl.edu and jes@sanger.ac.uk

regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from This sequence was finished as follows unless otherwise noted: all more than one m13 subclone.

http://www.wormbase.org/db/seq/sequence?name=Y58G8A;class=Sequence For a graphical representation of this clone sequence and its analysis see:

NEIGHBORING CLONE INFORMATION

The 5' clone is R02C2, 3100 bp overlap; the 3' clone is F33E11, 200 bp overlap. Actual start of this clone is at base position 20847 of DC2; actual end is at 7365 of T22H9.

NOTES:

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program [Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE INDEX.html) and The C. elegans ORFsome cloning project (http://wrfdb.dfci.harvard.edu/), elmilarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

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/strain="Bristol N2"
                                                                               /db xref="taxon:6239"
1. .34544
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source

FEATURES

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/ (db_xref="G1:73312127"
/ (db_xref="G1:73127"
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QKKWRKLEYQLLHIKRFAFFFYRTLINDRNSRADLSBRSETLGWPDSEKTQKE
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(Reverse transcriptase (RNA-dependent DNA polymerase))"
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complement (joint(13941. .14019,14622. .14785))
/locus tag="Y58G8A.5"
fatandard name="Y58G8A.5"
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Pred. No. 2.3e-85;
0; Mismatches 0; Indels 96;
                                                                                                            join(2379, .2443,2939, .3603,3779, .5358)
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Caenorhabbitis elegans clone Y108G3c, *** SEQUENCING IN PROGRESS
***, 2 unordered pleces.
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21366 CCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAGAAACT 21307
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis
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2 the traction, R. H.
Direct Submission
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/mol_type="genomic DNA"
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Waterston, R.H.
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Lowery, D.E., Geary, T.G., Kubiak, T.M. and Larsen, M.J.
Lowery, D.E., Geary, T.G., Kubiak, T.M. and Larsen, M.J.
G protein-coupled receptor-like receptors and modulators thereof
Patent: US 6632621-A 21 14-0CT-2003;
Pharmacia & Upjohn Company; Kalamazoo, MI
Location/Qualifiers
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Length 195349;
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TITLE G protein-coupled receptor-like receptors and modulators thereof JOURNAL Patent: WO 0138533-A 21 31-MX-2001; FEATURES Location/Qualifiers 1. 1130 Corganism="Homo sapiens" Mol type="unassigned DNA" Location/Dualifiers Mol type="unassigned DNA" Location/Dualifiers Mol type="unassigned DNA" Location-Coupled DNA" Lanslation-WNGSDCLALNSELWIYREDLSSRWYIMLVFAFLYLIIAAGIIG Lanslation-WNGSDCLALNSELWIYREDLSSRWYIMLVFAFLYLIIIAAGIIG Lanslation-WNGSDCLALNSELWIYREMLIGHVVARACOUTICITATATION LADYEYLAGISLCFSTFFILIAISIDRILIARPHYQAVGVIAIICAFAATITEPI READYEYLPELIKGAFKCENDNWEWELSDQRIAYGRAFICANTSEKII GOSMILKGAFKCENDNWEWELSDQRIAYGRAFICANTSEKII LADYEYLPELIKTQEYIFGIATHCIAMTSTVWNPELIYAVANIQLRAAFIDLMPHWLRR	Ouery Match Best Local Similarity 47.0%; Pred. No. 1.2e-16; Best Local Similarity 47.0%; Pred. No. 1.2e-16; Matches 438; Conservative 0; Mismatches 454; Indels 39; Gaps 3; Oy 136 GARGATATACTGTAGACTTTACATCGATCAATCTTCACATTCTCTACGGGTTCCTG 195	Qy 316 TTCACAGCGATTCCAGTCACCATGGTACCAAGACTGGGCATTCGGGTCA 375 Db 232 TGCACATCTGCAACAATCCTGTTACGAGATCTTTGTGAGAGTCTTTGGAGGG 291 Qy 376 GTGATGTGCCATTTAGTTCCTTTGTCAATTCGTGTTTGTGACTTTGTGAGTTGGAGG 435 Db 292 GCTTTATGCCAATTGCACTTCATTGCTGGTATCGGGGTTTCACATTTCACA 351 Qy 436 CTCACTGCAATTGCACCATTCATTGCTGGTATCACGATTCCAACTTTCACA 351 Db 352 TTGACTGCAATTCCCATGACAGATACTCTTATCTGGATAGTCTCAACAATT 495 CQ 1	0.0 0.16 ACTCCATACTGCGGCGCATTTGCGAGGCGAAATAGTCGAAAG 675
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Lowery, D.B., Geary, T.G., Kubiak, T.M. and Larsen, M.J.

G protein-coupled receptor-like receptors and modulators thereof

Patent: US 6632621-A 35 14-007-2003;

Pharmacia & Upjohn Company; Kalamazoo, MI
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              748 AGACAAAGAACTAATAGAATGCTTATTGGTATGGTAGTCGCATTCGCTTGCAGCTGGATT
                                                                        CCTTTAACATTACTCAATTTGGTCAAAGATTTTTAAAAAAGAGCCCGAATGGCTAAAACGT
                                                                                                    CAATCITCACATTCCTCTACGGGTTCCTGTTTTGTATTAGGCATTTTTGGAAACGGCGGCG
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llarity 50.5%; Pred. No. 6e-13;
Conservative 0; Mismatches 200; Indels
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Sequence 35 from patent US 6632621.
AR408557
AR408557.1 GI:40158797
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SPGNIPACSQLLSTHFESTTRRSVTTTIPSSI"
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                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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G procein-coupled receptor-like receptors and modulators
Patent: WO 0138533-A 35 31-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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50.5%; Pred. No. 6e-13;
iive 0; Mismatches 200; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
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Sequence 35 from Patent WO0138533.
AXIS1250
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CTTTGTGTTACATCGCAATTGATAGATATCGAAGTATTGTGACGCCACTCCGGGAACCAT 412
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                     815 TGAATTTGTTCAGAGATCTCGGAA
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                                                                                                                                                GI:14533396
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Unknown.
Unclassified.
I (bases 1 to 1352)
Lowery, D.B., Geary, T.G., Kubiak, T.M. and Larsen, M.J.
G protein-coupled receptor-like receptors and modulators thereof Patent: US 6632621-A 15 14-OCT-2003,
Pharmacia & Upjohn Company; Kalamazoo, MI
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        TCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCC
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               GI:40158788
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LVPTCQAFSVLISSWSLCYIAIDRYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYP
LYYSQNLKTWVIENVTLCGDFCGEFNWQSDEISKLTYTTSLLIIQLIIPAIIMSFCYL
22-JUN-2001
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TWLTNARRHTNVGVLSFFTBSFSVSVYYRRTLERHLGVNHFRRGTLADPTCTSBERSL
PRELQSNCFLLVPLMPLCQSVTRKNSHLAINRDGIVIPQANGSSRFPSSVNTNSTRDW
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                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                            Lowery, D.E., Geary, T.G., Kubiak, T.M. and Larsen, M.J. g protein-coupled receptor-like receptors and modulators thereof Patent: WO 0138533-A 15 31-MAY-2001; PHARMACIA & UPJOHN COMPANY (US)
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linear
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AP073925 13.15 bp DNA linear VRT 10-AUG-2000 Gadus morhua neuropeptide Y/peptide YY receptor Yb (NPXRb) gene,
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Arvidsson, A.-K., Mraith, A., Jonsson-Rylander, A.-C. and Larhammar, D. Direct Submission
Direct Submission
Submitted (23-UNN-1998) Neuroscience, Uppsala University, Box 593, Uppsala SE-75123, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotan, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Paracanthopterygii, Gadiformes, Gadidae, Gadus.

(bases i to 1315)
Arvidsson, A.K., Waith, A., Jonsson-Rylander, A.C. and Larhammar, D. Arvidsson, A.K. and Larhammar, D. Cloning of a neuropeptide Y/peptide YY receptor from the Atlantic cod: the Yb receptor

Regul, Pept. 75-76, 39-43 (1998)
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                                                                AICTACCGTAICTTATGTCTTTCGAGCACGTCGAIGGAAGCTTTTACGTTCAGCCCGGAG 613
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755 TGTACGIGTTGATTCTAATGGTTATTGTTTTTATGGCTTGCTGGTTCCCGTTGTCCGCCG
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                                                                                                                                                AAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGGGAAAATAGTCGAA
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<72. .>1196
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Plipligliaacylsiptlerromurrardssrdnrakoksriinvmlosivalayvey
lelnifantypomhhelmvscornlipsvchlvamastcvnpvvygflinsnpokchat
lshcrcwgaarryendplsavstbvtkbshmskssishs
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45.0%; Pred. No. 9.5e-09;
tive 0; Mismatches 322;
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53, Conservative
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us-10-650-467-104.rst

Perfect score:

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Scoring table:

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Minimum DB Maximum DB

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AY409053 Home sapi
BX617017 BX617017
BF286067 BST450658
CB741495 AMGNNUC:C
BX138447 BX738447
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BX938057 JGI AOKF8
BX982513 JGI AOKF8
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BX982514 JGI AOKF8
BX985306 JGI AOKF8
BX983058 JGI AOKF8
                                                                                                                                                                                                                                                                                                                                                                                   CV124545 801 bp mRNA linear EST 31-AUG-2004
OSTF30030H01 pDONR201 Entry vector Caenorhabditis elegans cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotta, Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (Dases I to 801)
Lamesch, P., Milstein, S., Hao, T., Rosenberg, J., Li, N., Sequerra, R.,
Bosak, S., Doucette-Stamm, L., Vandenhaute, J., Hill, D. B. and Vidal, M.
C. elegans ORFeome Version 3.1: Increasing the coverage of ORFeome resources with improved gene predictions
Genome Res. (ORFeome issue) (2004) In press
Contact: Philippe Lamesch and Tong Hao
                                                                                                                                                                                                                                                                                AL185971 Tetraodon
                                                                         AY413581 Pan trogl
AY413580 Homo sapi
                                   BU489814 604130606
CV024564 1977 Full
CO959636 AGENCOURT
             BJ144795 E
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| forganiem="Caenorhabditis elegans"
| fmol type="mRNA"
| ferrain="N2"
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lex="male and hermaphrodite"

/tissue_type="all tissues"

/dev_stage="all cells"

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Fax: 6176325739
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                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRimers FORWARD: TGGTTAGTTCGGCGGCCACCATT
                                                                     AY413581
AY413580
AX403053
BX617017
CD559637
BF286067
CB741495
BJ108410
BX738447
DR982313
DR982313
DR985315
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DR983058
CD559636
CNS028HM
A1943600
BJ144795
BP228990
BU489814
CV024564
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Caenorhabditis elegans
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Matches 702; Conservative
mRNA sequence.
CV124545
Query Match
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LOCUS
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AUTHORS
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BJ759866 BJ759866
BJ742720 BJ142720
BJ762291 BJ762291
BJ717135 BJ117135
BJ786750 BJ786750
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                             1 atggttagttcggcggccac......tgtgcaggcaactcttcta 1193
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Biocceleration Ltd.
                                                                                                                                                                                                                          41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
          GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                          nucleic search, using sw model
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BJ786750
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seq length: 200000000
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BJ759866 BJ759866 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone ykl532cl1 5', mRNA sequence.
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Caenorhabditis elegans
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (Dases 1 to 543)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
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                                                                        db xref="taxon:6239"
/clone="ykil66h04"
/sex="hermaphrodite"
/tssue_type="whole animal"
/dev stagge="L1"
/clone_lib="unpublished oligo-capped cDNA library,
elegans_L1 stage"
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                                                                                                                                                                                                              Score 579; DB 3; Length 615; Pred. No. 1.7e-160; 0; Mismatches 1; Indels
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'organism="Caenorhabditis elegans"
cocation/Qualifiers
                                          /mol_type="mRNA"
/strain="N2"
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BJ759866.1 GI:47599628
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Best Local Similarity 99.8
Matches 579; Conservative
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Kohara,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
                     CAACACTGATAAATCTACCGTATCTTATGTCTTTCCGAGCACGTCGATGGAAGCTTTTACG
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Eukaryota; Metazoa; Mematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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BJ113336.1 GI:18273407
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Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y., Shon-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y., And Sugano, S. A complementary view of the C.elegans genome Contact: Tadasu Shin-i Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Wishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Fax: 81-559-81-6855 Email: tshining-genes.nig.ac.jp.

Location/Qualifiers

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/clone="yk1187g06"
/tissue_type="whole animal"
/dev stage="ll"
/clone lib="unpublished oligo-capped cDNA library,
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                      Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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100.0%; Pred. No. 2.5e-128;
tive 0; Mismatches 0;
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/strain="N2"
      Caenorhabditis elegans
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                                                                                                                                                                                                                                                                           /tissue_type="whole animal"
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/clone_lib="unpublished oligo-capped cDNA library"
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                                                                                                                                                                                                                                                                                                                                                          Score 509; DB 3; Length 543;
Pred. No. 1.1e-139;
                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
            A complementary view of the C.elegans genome Unpublished (2002)
Contact: Tadasu Shin-i
Context: Tadasu Shin-i
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National Institute of Genetics
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Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                 1. 543
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/drain="N2"
/db xref="taxon:6239"
/clone="yk1532c11"
/sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                          42.7%; Scot.
100.0%; Pred. No. 1...
0; Mismatches
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BJ142720.1 GI:18302886
EST.
Caenorhabditis elegans
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Best Local Similarity 100.0
Matches 509; Conservative
Sugano, S.
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REFERENCE AUTHORS

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BJ786750 T13 bp mRNA linear EST 25-MAY-2004 BJ786750 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone ykl585h05 3', mRNA sequence.
BJ786750 GI:47665547 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 ATCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAAC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GGGGGGTACTATGGGGGGGGGGAACAACAGGGCTCCAATGGGTTCGCAACGTATTN 240
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                                                                                                                                                    A complementary view of the C.elegans genome
and Sugano, S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
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Fax: 81-55-81-6855
Fax: 10-55-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="L1"
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elegans L1 stage"
                                                                              Caenorhabditis elegans
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida;
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="whole animal"
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BJ117135.1 GI:18277247
EST.
                                                      Caenorhabditis elegans
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Robara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y. and Sugano, S.
A complementary view of the C.elegans genome
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/clone="yk1585h05"
/eex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="varied"
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36.5%; Score 435; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.1e-117;
Matches 435; Conservative 0; Mismatches 0; Indels

    .469
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Caenorhabditis elegans
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REFERENCE AUTHORS

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B1451132 530 bp mRNA linear EST 21-AUG-2001 kx1lb03.y3 Parastrongyloides trichosuri IL pAMP1 vl Chiapelli McCarter Parastrongyloides trichosuri cDNA 5' similar to WP:CE24480 Y58GBA.3 seven trans-membrane receptor ;, mRNA sequence. B1451132.1 GI:15275839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 TACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACCAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTC 183
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                                                                                               1 (bases 1 to 258)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
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Parastrongyloides trichosuri
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Parastrongyloides.

[ bases 1 to 530)
McCarter,J., Cliffon,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritcer,E., Bennett,J., Franklin,C.,
Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 AACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="whole animal"
/dev_stage="varied"
/clone_lib="unpublished oligo-capped cDNA library"
                                                                          Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                           A complementary view of the C.elegans genome Unpublished (2002)
Contact: Tadasu Shin-i
Contert: To Genetic Resource Information
National Institute of Genetics
1111 Yata, Mashima, Shizuoka 411-8540, Japan Pax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 257; DB 3;
Pred. No. 8.8e-65;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:6239"
/clone="yk1655f07"
                                                                                                                                                                                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                             Caenorhabditis elegans
Caenorhabditis elegans
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21.5%;
Best Local Similarity 99.6%;
Matches 257; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534
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                                                                                   1 (bases 1 to 713)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 AAAACGTTCCCGGACTGTCAAAAATACTCAACTCAACAGAGATTGTGTCCTCGTTTGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTTGTCACATTTATCGGGTGTTGGTTGCCTTTAACATTACTCAATTTGGTCAAAGATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:6239"
/clone="yk1585h65"
/clone="yk1585h65"
/tissue_type="whole animal"
/dev_stage="varied"
/clone_lib="unpublished oligo-capped cDNA library"
                                             Rukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.9%; Score 297; DB 3; Length 71
83.7%; Pred. No. 1.5e-76;
ive 0; Mismatches 0; Indels
                                                                                                                                              A complementary view of the C.elegans genome Unpublished (2002)
Contact: Tadasu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mashima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 259
                                                                                                                                                                                                                                                                                                                            Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
Caenorhabditis elegans
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 24.9
Best Local Similarity 83.7
Matches 381; Conservative
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Gaps

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123

180

240

DEFINITION ACCESSION VERSION

RESULT 8 BJ767176

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445 bp mRNA linear EST 24-JAN-2002 BJ153679 unpublished oligo-capped cDNA library, C. elegans Li stage Caenorhabditis elegans cDNA clone ykl322b09 3', mRNA sequence. BJ153679 BJ153679 GI:18321664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACACGACCTCCT 1148
                                                                                                                                                                                                                            BJ784215 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone yk1532c11 3', mRNA sequence.
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Kohara, Y., Shin-1, T., Thlerry-Mieg, J., Thierry-Mieg, D., Suzuki, Y. and Sugano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y. and Sugano, S.
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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Caenorhabditis elegans
Caenorhabditis elegans
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
I (Dases 1 to 477)
I (Dases 1 to 477)
I (Dases 1 to 477)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A complementary view of the C.elegans genome Unpublished (2002)
Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
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Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
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Pred. No. 1.1e-18;
0; Mismatches 2;
             920
                                                                         525
             886 ATCGGGTGTTGGTTGCCTTTAACATTACTCAATTT
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/tissue_type="whole animal"
/dev_stage="varied"
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Best Local Similarity 98.1
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jobes Vector: paMP1 (Gibco); Site 1: Not1; Site 2: Sal1; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The CDNA was made by using Dynabead oligo-dr priming (Dynal). PCR based library using a modified protocol from the SNART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the Unge sites of pAMP1. Nematodes were provided by Dr. Warwick Grant of AgRearch, New Zealand (warwick.grant@agresearch.co.nz).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             646 GCGAATTGGCAGAGCGAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAG 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TICGICGIGCCGAIGGCAGIGAICACGIATIGCIACTICAAAAICTIGCAAAAAGIGICA 765
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                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800

Fax: 314 286 1810

Fax: 314 286 
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCarn, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Infective Larvae"
/lab_host="DMIDS"
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(chiapeTl1 McCarter"
                                                                                                                                                                                                                                                                           63108, USA
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Pred. No. 7.3e-34;
0; Mismatches 216; Indels
                                                                                                                                                                      Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Parastrongyloides trichosuri"
/mol_type="mRNA"
/db_xref="taxon:131310"
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Best Local Similarity 57.5%;
Matches 296; Conservative (
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Reboul, J. Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotch, L., Bertin, N., Janky, R., Moore, T., Endress, G.M., Li, S., Jacotch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Paceek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans OrRecome version 1.1: experimental verification of the genome annotation and resource for protecome-scale protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CB402398 578 bp mRNA linear BST 15-MAY-2003
OSTF212A4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB402398
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Contact: Vidal M
Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5189

Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project: Contact david_hill@dfci.harvard.edu

marc vidal@dfci.harvard.edu

POLYĀ-No.
                                                                                                                                                                                                                                                                                                 152 ACTITIACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTT 211
                                                                                                                                                                                                                                                                                                                                               319 AATTGTTCGTCAAATCGGCGTTCACGCTCGTCTACGGCTTTCTGTTCATACTTGGTCTCG 260
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       Ancylostoma caninum genomic DNA was randomly sheared, end-repaired and size fractioned to enrich for 2-4 kb fragments. Genomic DNA was provided by John Hawdon (mtmin@gwumc.edu) at George Washington University. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."
                                                                                                                                                                                                                                                                                                                                                                                                 212 TTGGAAACGGCGCGCGTACTATGGGCGGTGGCGAGAACAAGGGGGCTCCAATCGGCTCGCA
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                       Length 608;
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/mol_type="mRNA"
/strain="N2"
                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                    Score 85.6; DB 10
Pred. No. 1.1e-13;
0; Mismatches 69
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/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="Ab-wrmcDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Matches 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
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Mitreva,M., McCatter,J.P., Pape,D., Ritter,E., Tsagareishvili,R., Ronko,I., Martin,J., Wylis,T., Dante,M., Meyer,R., Messina,D., Waterston,R.H., Clifton,S.W. and Wilson,R.
Genome Survey sequences from the parasitic nematode Ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole animal"
/dev_stage="11"
/clone_lib="unpublished oligo-capped cDNA library, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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library (AlAAGSS 001)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
M444 Forest Park Parkway, Box 8501, St. Louis, M0 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: nematode@watson.wustl.edu
Genomic DNA provided by John Hawdon (mtmjmh@gwumc.edu
sequenced by Washington University Genome Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151 CGACCTCTACTCCGACAGATGTGCAGGCAACTCTTTCTA 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 CGACCTNTACTCATTCGGACAGATGTGCAGGCAACTCTTTNTA 271
                                                                                                                                                                 1. .445
/organism="Caenorhabditis elegans"
/mol type="mRNA"
/strain="N2"
/db xref="taxon:6239"
/clone="ykl322b09"
Center For Genetic Resource Information
National Institute of Genetics
111 Onal Institute of Genetics
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 100; DB 3;
Pred. No. 5.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Ancylostoma caninum
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/strain="Baltimore"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Ancylostoma
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                                                                                                                                                                                                                                                                                                                   /sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/lab_host="GS10"
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CZ209081.1 GI:59212954
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Matches 100; Conservative (
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Best Local Similarity
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Conchocerca volvalus
Bukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.

1 (Dases 1 to 850)
Lizotte-Waniewski,M. and Williams,S.A.
Lizotte-Waniewski,M. and Williams,S.A.
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The CDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                             CAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCG 226
                                                                                                                                                                                                                                                                                                                                                                                                    TACTATIGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCA 286
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SWOVARCAP29C10SK Onchocerca volvulus adult female cDNA
(SAM98MLW-OVAR) Onchocerca volvulus cDNA clone SWOVARCAP29C10 5',
                                                                                                                                                                                                                                                                                                                                                 CGATTCTTGCAACCATCTACACTATAATTGTCGTAGTTGGCGTAACCGGCAATTTGTTAG
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                                                                                                                                                                                        7.0%; Score 84; DB 6; Length 578
50.5%; Pred. No. 3.3e-13;
tive 0; Mismatches 200; Indels
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/db_xref="taxon:6282"
/clone="SWOVAPCAP29C10"
/sex="female"
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Location/Qualifiers
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Email: genome@smith.edu
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/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humana: Two adult female worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult female mXNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) Followed by RNase H and DNA pol I. The library has 7 x 10E5 independent recombinants and the average rinsert size is ~1100bp.The library was constructed by Michelle Lizotte-Waniewski with worms provided by Michelle Lizotte-Waniewski with worms provided by Dr. Stara Lustigman. The library is available from Dr. Steven A. Williams, email: genome@smith.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB402411 537 bp mRNA linear BST 15-MAY-2003
OSTF212C1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB402411
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C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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/dev_stage="adult"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus adult female cDNA
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Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 850;
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Pred. No. 5.8e-12;
0; Mismatches 202; Indels
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                                                                         (SAW98MLM-OVAF) *
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Contact: Vidal M
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1..537
/organism="Caenorhabditis elegans"
/mol-type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/db_xref="taxon:6239"
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/fev stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA"
/note="
Marc Vidal Laboratory

Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180

Fax: 617 632 5739

Bmail: Marc Vidaledfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project: Contact david_hill@dfci.harvard.edu or POLYÃ-NO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 TIGACTGCAATCTCCATCGACAGATACATCCTGATTCGATTTCCGAAGGAAACCTATT 391
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Search completed: May 8, 2006, 17:59:20 Job time : 5407 secs

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May 8, 2006, 14:20:34 ; Search time 811 Seconds (without alignments) 9803.919 Million cell updates/sec
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   GenCore version 5.1.8
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Title: Perfect score:

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Searched:

Aba08967 Human GPC
Aav68484 Human 7-t
Aaa61230 DNA human 7-t
Aabk47410 Human CDN
Aax86955 Human NeV
Aby84708 Human NeV
Aby84708 Human NeV
Adv89683 Human NeU
Adv89683 Human NeU
Adv891327 Human Sof
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Adv91971 DmGPCRI C
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ADG8055
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ADG805198
AAC1968

ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_21:*

Database :

30L	
ID AAS072	AASO7253 standard; DNA; 1193 BP.
AC AAS07253;	53;
DT 12-SEP-2001	-2001 (first entry)
	G protein-coupled receptor-like (GPCR-like) receptor DNA #23.
	G protein-coupled receptor-like receptor: GPCR-like receptor: helminth:
KW endopa:	endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
•	
OS Homo sapiens	apiens.
	WO200138533-A2.
PD 31-MAY-2001	-2001.
	24-NOV-2000; 2000WO-US032225.
PR 24-NOV-1999;	-1999; 99US-0167523P.
	(PHAA) PHARMACIA & UPJOHN.
X	
PI LOWERY DE,	DE, Geary TG, Kubiak TM, Larsen MJ;
	WPI; 2001-343952/36.
DR P-PSDB	P-PSDB; AAU03851.
	Using G-protein-coupled receptor (GPCR)-like receptors to identify
	candidate compounds for the treatment and prevention of invertebrate
	parasites, especially helminths and insects.
	Claim 1; Page 173-175; 219pp; English.
	The sequence represents a DNA encoding a G protein-coupled receptor-like
	(GPCR-like) receptor protein. GPCR-like receptors and their associated
	nucleic acids may be used to identify candidate compounds for their
CC ability to	ability to modulate the activity of GPCRs. The sequences therefore are
	East transfill that properties and postings by analogous trail

Description

Query Match Length DB

Result No.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesequi980s:* genesequi990s:* genesequi000s:* genesequi001bs:* genesequi002as:* genesequi003as:* genesequi003as:*

Aas07253 G protein Aas07219 G protein Aas07210 G protein Aas07210 G protein Aas07210 G protein Aas7212 G protein Aag25892 Sequence Ad55872 Primary r Aa294667 Human neu Ad52876 Human neu Ad76145 Human neu Ad76145 Human neu Ada76145 Human neu Ada76145 Human neu Ada76145 Human neu Ad481010 Human neu Ad41210 Human neu

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                                                                       DB 4; Length 1193;
ectoparasitic invertebrate parasites, especially helminths and particularly ailments related to aberrant neurological neuromuscular function
                                               Sequence 1193 BP; 326 A; 281 C; 256 G; 330 T; 0 U; 0 Other;
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                                                                    100.0%; Score 1193;
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:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
neuromuscular disorder; human; nematode; ds.
                                   CAGCCGTTCTTCTTCTGGCCATAAATGCTCACGTCATAGCCCATGTCCTTAGTCGTCTGGAAC
                                                                                                                                                       CCTCTGCTATTCTTTTTGGCTGACACAAAACAAAAACGTTCCGGACTGTCAAAAATACTC
                                                                                                                                                                                                                                              1081 AACTCAACAGAGGTTCGAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC
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                                                                                                                                                                                                                                                                                                                                                                        1141 GACCTCCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
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The sequence represents a DNA encoding a G protein-coupled receptor-like (GPCR-like) receptor protein. GPCR-like receptors and their associated nucleic acids may be used to identify candidate compounds for their ability to modulate the activity of GPCRs. The sequences therefore are useful for treating and preventing infection by endoparasitic and ectoparasitic invertebrate parasites, especially helminths and insects, and particularly ailments related to aberrant neurological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                          G protein-coupled receptor-like receptor; GPCR-like receptor; helminth; endoparasite; ectoparasite; invertebrate; insect; neurological disorder; neuromuscular disorder; human; nematode; ds.
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                                  1447 GACCTCCTCCGACCTCTACTCCGACAGATGTGCAGGCAACTCTTTCTA
1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA
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                                                                                                                                                                                                                                    G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
neuromuscular disorder; human; nematode; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATT 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor-like receptor; GPCR-like receptor; helminth; endoparasite; ectoparasite; invertebrate; insect; neurological disorder; neuromuscular disorder; human; nematode; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGATTCTTGCAACCATCTACACTATAATTGTCGTAGTTGGCGTAACCGGCAATTTGTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 CTTTGTCAGTTTCTGACATTTTTGTGGCGATTGTTAGTGGTTCAGTAACGCCGATAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATTCTCTAAAGTTTGGTTATTTGGTGGACCATTGTGTCATTTACTACCTTTACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIGATCTICACCGATTIGATATIGGTGTTCACAGCGATTCCAGTCACACCATGGTACG
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                                                   Using G-protein-coupled receptor (GPCR)-like receptors to identify candidate compounds for the treatment and prevention of invertebrate parasites, especially helminths and insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 84; DB 4; Length 1098; Pred. No. 8.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor-like (GPCR-like) receptor DNA #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1098 BP; 280 A; 250 C; 230 G; 338 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 200; Indels
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                                                                                                                                                                     Claim 1; Page 139-141; 219pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      neuromuscular function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
P-PSDB; AAU03818.
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                                                   Using G-pro
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Best Local (
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240 GGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCAC 299
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                                                                                                                                              TGTACGTGTTGATTCTAATGGTTATTGTTTTATGGCTTGCTGGTTCCCGTTGTCCGCCG 814
CITITITGITATITAATGATICTACAAAAGGIACAAACCGACIGGCITGICGACGAGGGAI 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a DNA encoding a G protein-coupled receptor-like (GPCR-like) receptor protein. GPCR-like receptors and their associated nucleic acids may be used to identify candidate compounds for their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
neuromuscular disorder; human; nematode; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ability to modulate the activity of GPCRs. The sequences therefore are useful for treating and preventing infection by endoparasitic and ectoparasitic invertebrate parasites, especially helminths and insects, and particularly aliments related to aberrant neurological and neuromuscular function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TTCGAAAGCGACGAGTGA
                                                                                                                        TCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGAAAGAAGAAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Using G-protein-coupled receptor (GPCR)-like receptors to identify candidate compounds for the treatment and prevention of invertebrate parasites, especially helminths and insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor-like (GPCR-like) receptor DNA #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1374 BP; 402 A; 280 C; 296 G; 396 T; 0 U; 0 Other;
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Pred. No. 2.3e-09;
); Mismatches 199;
                                                                                ccargrigacingcegcacaacagecineaaacageae-
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                                                                                                                                                                                                         937
                                                                                                                                                                                                                                             rcaarrrcrrcagagarcrcggaa 838
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACTTTCCGTGGC---AAACATATTCTTGATAAACCTGGCAGTTTCTGATTTGCTTCTTT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCATCACGGCGCGGTGCCGATCACTCCAGTATTGGCGTTTTATGAAGCGATGCATATTTGGAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITIGIGITACATCGCAATIGATAGATATCGAAGTATIGIGACGCCACTCCGGGAACCAT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 ATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAG 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGICACATIATGIGGAGATTITTGCGGCGAGTICAATTGGCAGTCGGATGAAATAICCA 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                734 ATTGCTACTTCAAAATCTTGCAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAAT 793
                                                                                                                                                                                                                                                                                                                              The sequence represents a DNA encoding a g protein-coupled receptor-like (GPCR-like) receptor protein. GPCR-like receptors and their associated nucleic acids may be used to identify candidate compounds for their ability to modulate the activity of GPCRs. The sequences therefore are useful for treating and preventing infection by endoparasitic and ectoparasitic invertebrate parasites, especially helminths and insects, and particularly aliments related to aberrant neurological and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581 AGTTGACATATACTACGAGTTTATTGATTATTCAGCTGATTATTCCAGCAATTATCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 TGTTTGTATTAGGCATTTTTGGAAACGGCGCGTACTATGGGCGGTGGCGAGAACAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 TAATTATGTGTAAATTGGTTCCAACTTGTCAGGCGTTTTCGGTGCTCATTTCTTCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GT-----TATCCTCTATATTACTCACAGAACTTGAAACAATGGTTATTGA-----AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                         Using G-protein-coupled receptor (GPCR)-like receptors to identify candidate compounds for the treatment and prevention of invertebrate parasites, especially helminths and insects.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.6%; Score 78.8; DB 4; Length 1352; 47.4%; Pred. No. 3.9e-13; tive 0; Mismatches 402; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 1352 BP; 337 A; 284 C; 307 G; 424 T; 0 U; 0 Other;
                                                                                                          Larsen MJ;
                                                                                                                                                                                                                                                                                              Claim 1, Page 108-110; 219pp; English.
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                                                                                                            Kubiak
                         99US-0167523P
                                                                 (PHAA ) PHARMACIA & UPJOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 381, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuromuscular function
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                                                                                                                                                  WPI; 2001-343952/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                       P-PSDB; AAU03809
                           24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                225 CGTACTATGGGCGGTGGCGAGAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
                                                                                                                                                                                                                                                                                                                                                                                                 621 CAGCCTGGCTCTGGGAGATCTGCTACATCATCATCGACATTCCCATTAATGCCTACAA 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 GCTGCTGGCAGGGGACTGCCATTTGGAGCTGAGATGTGCAAGCTGGTGCCCTTCATACA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGGCTTCTGTGGGGATCACAGTGTTCTATGTGCTCTAAGTATTGACAGATATC 799
                monkey COS-7 cells using mammalian expression vector pCDMB, which contains a replicating initiation point of SV40 and polyoma, and another replication initiation point of cytomegalovirus polymens and another prom, oter and M13. The cells expressing biologically active endothelin receptor were identified by incubating transfected COS-7 cells in culture containing [1251- Tyr13] endothelin-1, and detecting with X-ray film. Positive calls were then rescreened, a clone isolated and its sequence of insertion fragments analysed to determine the CDNA sequence of rat endothelin receptor. See also AAR25394. (Updated on 25-MAR-2003 t
     expression of mRNA from DNA fragments accumulated in
                                                                                                                                                                                                                                                                                                                                          561 ACTGCTAAGAATCATCTACAAGAACAAGTGCCATGAGAAATGGTCCCAATATCTTGATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3414.
                                                                                                                                                                                                                                                        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG
                                                                                                                                                                                                                                                                                                                                                                      CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA
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                                                                                                                                                                                                   Length 1965;
                                                                                                                                                                        Sequence 1965 BP; 529 A; 467 C; 467 G; 502 T; 0 U; 0 Other;
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                                                                                                                                                                                                                               148;
                                                                                                                                                                                                  Score 62.2; DB 2;
Pred. No. 6.4e-08;
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2002US-0363534P.
2002US-0370248P.
2002US-0371134P.
2002US-0371135P.
2002US-0371135P.
2002US-037135P.
                                                                                                                                                                                                  5.2%;
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2002US-0378370P.
2002US-0378652P.
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                                                                                                                                                                                                                            151; Conservative
    d by direct
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Best Local Similarity
                                                                                                                                            correct PR field.)
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08-APR-2002;
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10-APR-2002;
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19-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - new agents contg. the receptor are or hypotension.
                           CGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGA
                                                      CGATTGCATGATGTGCATATTATCGCTTCCAATCACTCCAATCACAAAAA
                                                                                                 TGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC
                                                                                                                                                                                                                        393 ACATTCTACACCACTATCCCAAAGAGGAGCATTTCTTACTACTCTATTCTGAGGATCCT
                                                                                CTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTT
                                                                                                                                                                                              480 CACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vasoconstrictor peptide; endothelial cells; hypertension;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was deduced as follows. A cDNA library was prepared by reverse transcription of polyA RNA isolated from rat lung. This was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "endothelin_receptor"
                                                                                                                                                                                                                                                                               CrcrrrrgirgiaAcrcraccrar 477
                                                                                                                                                                                                                                                    CTCAACACTGATAAATCTACCGTAT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encodes endothelin receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding endothelin receptors useful in diagnosing hypertension
                                                                                                                                                                                                                                                                                                                                                    AAQ25892 standard; cDNA; 1965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus rattus.
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23-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endothelin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barafotoxin
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The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatocoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTACTATGGGCGGTGGCGAGAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
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                                                                                                                                                                                                                                                                                                                      Castle A,
                                                                                                                                                                                                                                                                                                                      Higgs B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 44; SEQ ID NO 3414; 874pp; English.
                                                                                                                                                                                                                                                                                                                      Johnson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.2%;
                          2002US-0378665P.
2002US-0394230P.
2002US-0394253P.
                                                                                                                               04-SEP-2002; 2002US-0407688P.
2002US-0378653P
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                                                                                                                                                                                                                                                                                                                  Porter M,
                                                                                                                                                                                                                                               LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-731472/69.
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Best Local Similarity
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                             09-MAY-2002;
                                                                                                                                                                                                                                                                                                                  Mendrick D,
Elashoff M;
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The present sequence is that of human neuropeptide FF (NPFE2) receptor CC cDNA, isolated from spleen cDNA by 5/3'RACE. The cDNA contained in planal, isolated from spleen cDNA by 5/3'RACE. The cDNA contained in planal, indicating a role in gestational contained in the placenta, indicating a role in gestational contained in the placenta, indicating a role in gestational contained in the regulation of fear, pain modulation of learning and memory and in the regulation of fear, pain modulation of learning and memory and in the regulation of fear, pain and analgesia, and may provide a target for treatment of depression, anxiety, phobias and mood of gestates. Incalisation to the requlation of extrapyramidal motor disorders. Localisation to the requlation of extrapyramidal motor contains. The invention provides rat and human NPFF polypeptides and antisense oligonuclectides, recretors, methods of treating an abnormality associated mammalian NPFF receptors, methods of treating an abnormality associated continuation of the requirement of compounds of the reating an abnormality involve administering an indicating an abnormality involve administering an increasing/decreasing NPFF activity involve administering an another continuation principarine release disorder, a gastrointestinal disorder, irritable bowel syndrome, a cardiovascular disorder; an electrolyte continuation and transmission, diabetes and mammary and present of disorder, an enemory enemory contained in disorder, an enemory enemory contained in disorder, an enemory enemory enemory contained and enemory enemory enemory contained enemory enemory contained enemory enemo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding a mammalian neuropeptide FF (NPFF) receptor, useful for treatment of e.g pain, obesity, diabetes, hypertension, hypotension, hypoglycemia, respiratory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coordination disorder, a sensory integration disorder, obesity, pain, psychotic behaviour, morphine tolerance, nicotine addiction, opiate addiction, affective disorder or migraine (all claimed)
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                                    nootropic; neuroprotective; analgesic; anoretic; antipsychotic; antiaddictive; antimigraine; hypertenalve; hypotensive; cardiant; antiasthmatic; gene therapy; plasmid cDNA3.1-hNPFF2b; g protein coupled receptor; ss.
Neuropeptide FF receptor; NPFF2 receptor; human; antiinflammatory antiasthmatic; antidiabetic; immunostimulant; immunosuppressive;
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Pred. No. 8e-08;
0; Mismatches 234; Indels
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                                                                                                                                                                                                                   Location/Qualifiers
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Human neuropeptide FF (NPFF2) receptor cDNA.

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB; gene; neuropeptide FF receptor; interstitial cystitis; steroid hormone disorder; gastrointestinal disorder; hypotension; diabetes; hypotension; hypoglycaemia; reproductive function disorder; obesity; morphine tolerance; cognitive disorder; immune disorder; irritable bowel syndrome; migraine; cardiovascular disorder; memory disorder; motor integration disorder; human; NPPF.
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                                                                                   CAACTIGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACCATGGTA
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The invention relates to isolated nucleic acids encoding neuropeptide FF (NPFF) receptors. Also described is a method involving competitive binding for identifying a chemical compound which specifically binds to human Neuropeptide FF (NPFE) receptor. The compound identified by the method is useful for treating interstitial cystitis, steroid hormone disorder, psatrointestimal disorder, hypotension, diabetes, hypostrension, hypostyroamia, reproductive function disorder, obesity, morphine migraine, cardiovascular disorder, memory disorder, irritable bowel syndrome, migraine, cardiovascular disorder, memory disorder and motor integration disorder. The present sequence represents cDNA encoding human neuropeptide FF receptor, hNPFF2D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a neuropeptide FF (NPFF) receptor proteins and their DNA. The invention is useful for diagnosing or treating a disorder, e.g. diuresis, cardiovascular conditions such as hypertension, hypotension and congestive heart failure, memory loss, affective disorders, schizophrenia, pain, locomotor problems, circadian rhythm disorders, eating/body weight disorders, sexual/reproductive disorders nasal congestion, diarrhea, gastrointiestinal disorders, or disorders of the lower urinary tract. The invention is also useful in gene therapy. The present sequence is the human neuropeptide FP2 (NPFP2) receptor protein encoding DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a human or rat neuropeptide FP2 receptor, useful for diagnosing or treating a disorder, e.g. cardiovascular, affective, reproductive, gastrointestinal, or lower urinary tract
                                                           "Human neuropeptide FF2 (NPFF2) receptor
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22-FEB-1999;
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Preparing a composition that specifically binds to mammalian neuropeptide FF (NPFF) receptor, comprises determining if the assertations of the company of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; genitourinary; disease; gastrointestinal disease; gastrointestinal disease; gastrointestinal disease; gastrointestinal-gen.; cardiovascular disease; cardiovascular-gen.; hypotensive; hypotensive; antidiabetic; metabolic disorder; respiratory disease; respiratory-gen.; antiasthmatic; inflammation; endocrine disease; immune disorder; immunemodulator; endocrine-gen.; muscular-gen; osteopethic; cognitive disorder; nootropic; neurological disease; memory disorder; anorectic; notropic; analgesic; antismoking; psychiatric disorder; toxicity and intoxication; antiaddictive; antimigraine; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human NPFF receptor (NPFF2b) protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuropeptide FF receptor, urinary tract disease; uropathic;
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22-FEB-1999; 99US-00255368.
24-SEP-1999; 99US-00405558.
29-MAR-2000; 2000US-00538036.
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disorder, an immune disorder, an endocrine disorder, a musculoskeletal disorder, a cognitive disorder, a memory disorder, obesity, pain, nicotine addiction, opiate addiction or migraine. The present sequence the human NPFF receptor (NPFF2b; NPFF2) DNA.
                                                                                                               165 ATCAATCTTCACATTCCTCTACGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCG
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tive 0; Mismatches 234; Indels
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Novel polynucleotide encoding G protein coupled receptor A4, useful for producing recombinant cell lines for discovering therapeutic agents that modulate the receptor activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 234; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61.6; DB 3;
Pred. No. 8.4e-08;
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                                                                                                                                                                                                                                                         2; Fig 1; 59pp; English.
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al Similarity 46.3%;
202; Conservative
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The present invention relates to pharmaceutical compositions comprising
the coding sequences shown in ACH00815-ACH00827, or their encoded
proteins (shown in ABG75054, ABG75057). These are proteins
converted in the metabolism of triglycerides and in energy homeostasis,
cand their coding sequences. The composition is useful for the manufacture
of an agent for detecting, verifying, treating, alleviating or preventing
confusorders, including metabolic diseases such as obesity and other body-
weight regulation disorders as well as related disorders such as
confusorders, acting disorder, cachexia, diabetes mellitus,
hypertension, coronary heart disease, hypercholesterolaemia,
confusorders, osteoarthritis or galistones, in cells, cell masses,
confusorders are coding sequences can be used in the production of
transgenic animals which under- or over-produce the gene of interest. The
confusor control of control of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                               New pharmaceutical composition comprising a nucleic acid molecule encoding proteins regulating the energy homeostasis and metabolism of triglycerides useful for detecting or preventing metabolic diseases, e.g.
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                                                                                                                                                        14-MAR-2002; 2002EP-000058B2.
15-MAR-2002; 2002EP-00006512.
20-MAR-2002; 2002EP-00006571.
25-MAR-2002; 2002EP-00006810.
                                                                                                             14-MAR-2003; 2003WO-EP002714.
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                     WO2003075945-A2.
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Sequence 41470, A Sequence 41470, A Sequence 9, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 23, Appli Sequence 23, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 26, Appli Sequence 10, Appli Sequence 10, Appli Sequence 25, Appli Sequence 10, Appli

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GCGGCACAAGGCATCGATGATATACTGTAGACTTTTACATCCGATCAATCTTCACATC 180
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US-10-213-821-1
US-10-736-048-1
US-10-489-425-61
US-11-097-143-41471
US-11-097-143-41470
                                            ; OTHER INFORMATION: Clone identifier: CEGPCR19.2 US-10-650-467-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1193;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100
Matches 1193; Conservative
  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(1191)
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Sequence 399, App
Sequence 7, Appli
Sequence 4147, Ap
Sequence 8018, Ap
Sequence 7, Appli
Sequence 1, Appli
                                                               8, 2006, 14:37:08 ; Search time 1118 Seconds (without alignments) 8824.122 Million cell updates/sec
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3: /cgn2_6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*
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         GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-650-467-35
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APPLICANT: Kubiak, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: MODITATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 28341/62123
CURRENT APPLICATION NUMBER: US/10/650,467
CURRENT PILING DATE: 2003-08-28
PRIOR PILING DATE: CURRENT APPLICATION NUMBER: US/09/721,870
PRIOR FILING DATE: CURRENT PILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PALENT VET. 2.0
SEQ ID NO 39
LENGTH: 1500
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US-10-650-467-39
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100.0%; Score 1193;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches
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      CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG
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Sequence 39, Application US/10650467 Publication No. US20050176069A1 GENERAL INPORMATION: APPLICANT: Lowery, David E.

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                                           CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGGCCCGAATTGCCTAAAACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 106, Application US/10650467
Fublication No. US20050176069A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lowery, David E.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: MOULANDES OF G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 28341/6223
CURRENT PELING DATE: 2003-08-28
PRIOR PAPLICATION NUMBER: US/10/650,467
CURRENT FILING DATE: 2003-08-28
PRIOR PALING DATE: CURRENT APPLICATION NUMBER: US/09/721,870
PRIOR PAPLICATION NUMBER: CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIN Ver. 2.0
SSOFTWARE: DNA
TYPE: DNA
CURRANT: MANAGEMENT APPLICATION NUMBER: DNA
CORGANISM: Homo sapiens
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Best Local Similarity 94.2%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0;
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NAME/KEY: CDS
LOCATION: (1)..(1299)
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US-10-650-467-106
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                                         -----tritigigicagiacticaccidaaaactggggagcciatgaaaagcagagaaa 567
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Publication No. US20050176069A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOWERTY, Timothy G.
APPLICANT: APPLICANT: Timothy G.
APPLICANT: LOWERTH AND G.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 28341/6223
CURRENT APPLICATION NUMBER: US/10/650,467
CURRENT APPLICATION NUMBER: CIRRENT APPLICATION NUMBER: US/09/721,870
FRIOR PILING DATE: CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
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                                                                                     676 ATTIACGGAACTACGGTTATGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGTAT
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7.0%; Score 84; DB 9; Length 1090
Best Local Similarity 50.5%; Pred. No. 1.6e-14;
Matches 204; Conservative 0; Mismatches 200; Indels
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US-10-650-467-35
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US-10-650-467-35
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LENGTH: 1098
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                                1201 GGATCCAGCTACACGACCTCCCCCCGACCTCTACTATCGGACAGATGTGCAGGCAACT
                                                                                                                                                                                                                                                                                               APPLICANT: Lowery, David E.
APPLICANT: Lowery, David E.
APPLICANT: Geary, Timothy G.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Kubiak, Teresa M.
TITLE OF INVENTION: MOUNATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 28341/6223
CURRENT APPLICATION NUMBER: US/10/650,467
CURRENT FILING DATE: 2003-08-28
PRIOR PLING DATE: CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 1130
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US-10-650-467-21
                                                                                                                                                                                                                                          Sequence 21, Application US/10650467
Publication No. US20050176069A1
GENERAL INFORMATION:
                                                                                                                       1261 CTTTCTA 1267
                                                                                         CTTTCTA 1193
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PEATURE:
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                                                         353 crrigigiracárcecaarrearaeararceaagrariciaececcacreceegaacear 412
                                                                                                                                                                                                                    554 ATCTACCGIATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAG 613
                                                                                                                                                                                                                                                                      473 GT-----TATCCTCTATATTACTCACAGAACTTGAAAACAATGGTTATTGA-----AA 520
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        434 GCCTCACTGCAATCTCCTTAGATAATTTCTGCATATCAACGATCCCCACCAAACAACAG 493
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Sequence 25, Application US/10650467

Publication No. US20050176069A1

GENERAL INFORMATION:

APPLICANT: Lowery, David E.

APPLICANT: Rubiak, Teresa M.

APPLICANT: Larsen, Martha J.

TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS

FILE REPREBACE: 28341/6223

CURRENT FILING DATE: 2003-08-28

PRIOR FILING DATE: 2003-08-28

PRIOR PLLING DATE: CURRENT PILING DATE: 2000-11-24

NUMBER OF SEQ ID NOS: 180

SOFTWARE: PARENTIN VET: 2.0

SOFTWARE: PARENTIN VET: 2.0
                                                                                                              TITCIATICGICAAGCGITGGCAATAACATITCTTATCTGGATAGICTCAACACTGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                             674 AGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGT
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Pred. No. 4.4e-09;
0; Mismatches 199; Indels
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Best Local Similarity 48.3%;
Matches 186; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1)..(1371)
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                                                                                                                                                                                                                 466
                                                                                                                                                                                                                                                                                                                                                   ACTIGATCTICACCGATTIGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACG 346
                                                                                                        CGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATT 406
                                                                                                                                                                                                                                                             GTACCGCGTTGAGTTTTTCCACGTTAACGCTCACCGCAATTGCAATTGACAGATATTC 385
                                                                                                                                                                                                                                                                                                                  467 ATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 TCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 rcaardarradacacrecretrraaagrececrecararreagracraracrec 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 TGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAACAAGC 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 GGCTCCAATCGCCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGG 313
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                                                 206 CTTTGTCAGTTTCTGACATTTTTGTGGCGATTGTTAGTGGTTCAGTAACGCCGATAACCG
                                                                                                                                                                                                            407 CGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCCTTAGATAAATTTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lowery, David B.

APPLICANT: Geary, Timothy G.

APPLICANT: Geary, Timothy G.

APPLICANT: Wibiak, Timothy G.

APPLICANT: Larsen, Martha J.

TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 28341/6223

CURRENT APPLICATION NUMBER: US/10/650,467

CURRENT APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870

PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870

PRIOR PRILING DATE: CURRENT FILING DATE: 2000-11-24

NUMBER OF SEQ ID NOS: 180

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15.

LENGTH: 1352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 TCAACAGCGCCATCTCAGTTGGGCTTTCGGTACCATTATTCATG 489
                                                                                                                                                                                                                                                                                                                                                                                                                     527 TTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570
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US-10-650-467-15
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Publication No. US20050176069A1
GENERAL INFORMATION:
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FEATURE:
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APPLICANT: Jones, Kenneth A.
APPLICANT: Jones, Kenneth A.
APPLICANT: Bonoini, James A.
APPLICANT: Bonoini, James A.
APPLICANT: Bonowsky, Beth B.
APPLICANT: Bonowsky, Beth B.
APPLICANT: Craig, Douglas A.
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
FILE REFERENCE: 57155-D/JPW
CURRENT APPLICATION NUMBER: US/09/538,036
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
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524
                                                                                                                                                        525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584
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GCATATCAACGATCCCACCAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT
                                                  465 grorigiogrichaccerritaaaccaaaacricaaaaacaacaacairirgicarratar
                                                                                                           525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT
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46.3%; Pred. No. 1.5e-07;
iive 0; Mismatches 234;
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10992407; Publication No. US20050089937A1; GENERAL INFORMATION, Christophe P.G. APPLICANT: Jones, Kenneth A.
                                                                                                                                                                                                                   585 CGATGGAAGCTTTTAC 600
                                                                                                                                                                                                                                                                        585 AGAAGAAAAATATTAC 600
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Matches 202
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Publication No. US20020198367A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Jones, Kenneth A.
APPLICANT: Borowsky, Beth
APPLICANT: Borowsky, Beth
TITLE OF INVENTION: And Uses Thereof
FILE REPERENCE: 1795/57155-A
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                                                     CGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGA
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/161,113
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VET. 2.0 - beta
SEQ ID NO 5
LENGTH: 1302
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US-09-866-248A-5
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US-09-866-248A-5
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                                                                                                                                                                                                                                                                                       Score 61.6; DB 10; Length
Pred. No. 1.6e-07;
0; Mismatches 234; Indels
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Publication No. US20030139589A1
GENERAL INFORMATION:
APPLICANT Zastawny, Roman
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR A4
FILE REPRERCES: 2931-104
CURRENT APPLICATION NUMBER: US/10/060,369
CURRENT PILING DATE: 2003-03-31
PRIOR PILING DATE: 1998-08-16
NUMBER OF SEQ ID NOS: 12
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46.3%; Pred. No. 1.6e-07;
tive 0; Mismatches 234;
    TITLE OF INVENTION: Target Genes FILE REFERENCE: AM101083 (031896-042000) CURRENT APPLICATION NUMBER: US/11/060,756 CURRENT FILING DATE: 2005-02-18 NUMBER OF SEQ ID NOS: 303284 SOFTWARE: Patentin version 3.2 SQTWARE: Pat
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Best Local Similarity 46.3
Matches 202; Conservative
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Matches 202; Conservative
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; ORGANISM: Human
US-10-060-369-8
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                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REPERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
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Sequence 6763, Application US/11060756

PUBLICATION NO. US20050221354A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, Milliam Martin
APPLICANT: Mounts, Milliam Martin
APPLICANT: Mounts, Milliam Martin
525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584
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Pred. No. 1.6e-07;
0; Mismatches 234;
                                                                                                                                                                                                                                    Sequence 2491, Application US/11060756
Publication No. US200S0221354A1
GENERAL INFORMATION:
                                                                        CGATGGAAGCTTTTAC 600
                                                                                                                  585 AGAAGAAAAATATTAC 600
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Best Local Similarity 46.3%;
Matches 202; Conservative
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LENGTH: 1400
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                       CGTACTATGGGCGGTGGCGAGAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT
                                                                                  242 geittegeittattgiaatgaggaacaacatatgekeekeeneeraaterietieti
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APPLICANT Bavis, Robert E.
APPLICANT Davis, Robert E.
APPLICANT Gardell, Luis Roberto
APPLICANT Gardell, Luis Roberto
APPLICANT Gardell, Luis Roberto
APPLICANT Lameh, Jelveh
APPLICANT Lameh, Jelveh
TITLE OF INVENTION: TREATING NEUROPATHIC PAIN WITH
TITLE OF INVENTION: TREATING NEUROPEPTIDE FF RECEPTOR 2 AGONISTS
FILER REFERENCE: ACADIA.038A
CURRENT APPLICATION NUMBER: US/10/949,140
CURRENT PILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: 60/508,008
PRIOR PILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-09-25
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Pred. No. 1.7e-07;
0; Mismatches 234; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     585 CGATGGAAGCTTTTAC 600
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Similarity 46.3%;
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US-10-949-140-1
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Best Local
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APPLICANT: BLUELBY, Arabeter
APPLICANT: Broenner, Chenter
TITLE OF INVENTION: GG927, CG10823, CG18418, CG15862, CG3768, CG11447 and CG16750
TITLE OF INVENTION: Homeostasis
FILE OF INVENTION: Homeostasis
FILE OF INVENTION: Homeostasis
FILE REFERENCE: 2923-651
CURRENT PILING DATE: 2004-09-14
FRICK FILING DATE: 2003-03-14
FRICK FILING DATE: 2003-03-14
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ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG
                                                          255 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTTGTGCATGATGGGAAATACTGT
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Publication No. US20050119206A1
GENERAL INFORMATION:
APPLICANT: Rulenberg, Karsten
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ORGANISM: Homo sapiens
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US-10-507-617-4
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Sequence 743, Application US/10276774

Sequence 743, Application US/10276774

Sequence 743, Application US/2040053245A1

GENERAL INPORMATION:

APPLICANT: Hyeeq, Inc.

APPLICANT: Tang, Y, Tom et al

TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides

FILE REPRENCE: 21272-030

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SEQ ID NO 743

LENGTH: 1824
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                                                                               TICGIGIICGGIGITIGIGACGAGIIGGAGCCICACIGCAAICICCITAGAIAAATITICI 464
                                                                                                                                                                            422 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 481
                                                                                                                                                                                                                          465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
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AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 361
                                                                                                                                                                                                                                                                                                                                                                   542 GATCÁTCTGGGTCCTAGCCATCACCÁTTÁTGTCTCCATCTGCAGTAATGTTACÁTGTGCA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
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                                             CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGTGTGCCATTTAGTTCCTTTGTCAAA
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2424, Ap	Sequence 5, Appli Sequence 1, Appli	'n	25,	-	Sequence 33, Appl		Sequence 38, Appl	Sequence 1, Appli	Sequence 4059, Ap	Sequence 594, App	594,	3736
SUMMARIBS	US-11-136-527-2424	US-10-992-5//-5 US-10-510-018-1	US-11-183-615-3	US-11-080-991-25	US-10-960-414-9	US-11-100-640-33	US-10-473-173-20	US-11-223-294-38	US-10-992-577-1	US-11-136-527-4059	US-11-224-663-594	US-11-224-525-594	US-11-136-527-3736
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% Query Match Length DB	2025	1936	1605	1888	2752	1329	1578	1299	1410	3219	3219	3219	3295
& Query Match	5.2	. v.	4.8	4.8	4.8	4.5	4.5	4.2	4.2	4.1	4.1	4.1	4.1
Score	62.2	61.6	57.8	57.8	57.8	53.4	53.4	20	20	48.8	48.8	48.8	48.8
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US-11-136-527-2750 US-11-136-527-2754 US-11-136-527-231 US-11-136-527-331 US-11-136-527-3742 US-11-136-527-3742 US-11-136-527-3742 US-11-136-527-3742 US-11-136-51-16 US-11-183-615-6 US-11-183-615-16 US-11-183-615-16 US-11-136-527-3122 US-11-136-527-3122 US-11-136-527-3122 US-11-136-527-3122 US-11-136-527-3122 US-11-136-527-3123 US-11-136-527-3131 US-11-137-527-3131 US-11-137-527-3131 US-11-137-527-4061	11-224-525-59 -11-224-525-59 -11-136-527-35 -11-136-527-22 -11-233-294-55 -10-992-577-7
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ALIGNMENTS

554 ATACATCAACACGATTGTATCATGCCTCGTGTTCGTGCTAGGCATCATCGGGAACTCCAC 613 674 CAGCCTGGGTCTGGGAGATCTGCTACACATCATCGACATTCCCATTAATGCCTACACAA 733 225 CGTACTATGGGCGGTGGCGAGAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284 614 ACTGCTAAGAATCATCTACAAGAACAAGTGCATGAGAAATGGTCCCAATATCTTGATCGC 673 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344 165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG Gaps ; 0 DB 17; Length 2025; Query Match 5.2%; Score 62.2; DB 17; Length Best Local Similarity 50.5%; Pred. No. 5e-07; Matches 151; Conservative 0; Mismatches 148; Indels ; TYPE: DNA ; ORGANISM: Rattus norvegicus US-11-136-527-2424 US-11-136-527-2424 285 셤 ઠ ሯ ď à 셤

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Pred. No. 7.3e-07;
0; Mismatches 234;
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Publication No. US20060040964A1
GENERAL INFORMATION:
BAPLICANT: Bakthavacchalam, Rajagopal
APPLICANT: Blum, Charles A.
                                                                                                                                                                                ; Sequence 1, Application US/10510018; Publication No. US20050244896A1; GENERAL INFORMATION:
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5.2%;
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Best Local Similarity 46.3<sup>3</sup>
Matches 202; Conservative
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APPLICANT: Jones, Kenneth A.
APPLICANT: Jones, Kenneth A.
APPLICANT: Bondini, James A.
APPLICANT: Borowsky, Beth B.
APPLICANT: Borowsky, Beth B.
APPLICANT: Craig, Douglas A.
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
TITLE OF INVENTION: UNABER: US/10/992,577
TITLE OF INVENTION: UNABER: US/09/538,036
FRIOR FILING DATE: 2004-11-18
FRIOR PRICATION NUMBER: US/09/558
FRIOR APPLICATION NUMBER: US/09/558
FRIOR PRICATION DATE: 1999-09-24
FRIOR APPLICATION NUMBER: US/05/558
FRIOR PRILING DATE: 1999-09-25
FRIOR APPLICATION NUMBER: US/11,113
FRIOR PRILING DATE: 1990-09-25
FRIOR PRILING DATE: 1990-09-25
FRIOR PRILING DATE: US/09/161,113
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FRIOR PRILING DATE: US/09/161,113
FRIOR PRILING DATE: US/09-09-25
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                                            734 GCTGCTGGCAGGGGACTGGCCATTTGGAGCTGAGATGTGCAAGCTGGTGCCSTTCATACA 793
      CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
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Pred. No. 6.4e-07;
                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10992577
Publication No. US20050260687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             585 CGATGGAAGCTTTTAC 600
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Best Local Similarity 46.3%;
Matches 202; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Publication No. US20060074565A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MILLER, LANCE D.
APPLICANT: GEORGE, JOSHY
APPLICANT: WEGA, VINGENSIUS B.
TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
TITLE OF INVENTION: PROGNOSIS, AND DIAGNOSIS OF CANCERS
FILE REFERENCE: 38271-76067
CURRENT PLING DATE: 2004-10-06
NUMBER OF SEQ ID NOS: 500
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT
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                                                                                                                                                                                                                                                                                                                                                            Length 1888;
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                                                                                                                                                                                                                                                                                                                                              4.8%; Score 5....
46.4%; Pred. No. 8.9e-06;
....ve 0; Mismatches 217; Indels
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46.4%; Pred. No. 1e-05;
tive 0; Mismatches 217;
             PRIOR FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                      NAME/KGY: misc feature
LOCATION: 1814, 1834, 1850
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 46.4
Matches 188; Conservative
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Best Local Similarity 46.44
Matches 188; Conservative
                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-10-960-414-9
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LENGTH: 2752
                                                                                       SEQ ID NO 25
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Publication No. US20050266437A1
GENERAL INFORMATION:
APPLICANT: Veiby, Petter Ole
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: AND OVARIAN CANCER
TITLE OF INVENTION: AND OVARIAN CANCER
TITLE APPLICATION NUMBER: US/11/080,991
CURRENT APPLICATION NUMBER: US/11/080,991
CURRENT PILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: US/10/176,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 AAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCGGCACAAGGCAT 134
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                                              APPLICANT: De Lombaert, Stephane W. APPLICANT: Tran, Jennifer W. APPLICANT: Tran, Jennifer W. APPLICANT: Tran, Jennifer W. APPLICANT: Zhong, Xiaozhang W. APPLICANT: Bliott, Richard L. APPLICANT: Hammond, Marlys L. TITLE OF INVENTION: SPIROISOBENZOFURAN-1,4'-PIPERIDIN]-3-ONES AND TITLE OP INVENTION: 314-SPIROISOBENZOFURAN-1,4'-PIPERIDINS AND
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Pred. No. 8.4e-06;
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                                                                                                                                                                                                                                                      TILE REFERENCE: U 014339-7
CURRENT APPLICATION NUMBER: US/11/183,615
CURRENT APPLICATION NUMBER: US/11/183,615
CURRENT APPLICATION NUMBER: US/0/410,648
PRIOR PILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: 10/013,846
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 2000-12-12
SOFTWARE: PatentIn version 3.1
Brielmann, Harry L.
Darrow, James W.
De Lombaert, Stephane W.
Hutchinson, Alan W.
Tran, Jennifer W.
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Best Local Similarity 46.4
Matches 188; Conservative
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TITLE OF INVENTION: Microarray Gene Expression Profilling in Clear Cell Renal Cell TITLE OF INVENTION: Microarray Gene Expression Profilling in Clear Cell Renal Cell TITLE OF INVENTION: Carcinoma. Prognosis and Drug Target Identification FILE REPERENCE: 38345-170094
CURRENT PAPLICATION NUMBER: US 60/219,411
PRIOR APPLICATION NUMBER: US 60/279,411
PRIOR PILING DATE: 2001-03-29
NUMBER OF EEQ ID NOS: 498
SOPTWARE: Patentin Version 3.2
SEQ ID NO 20
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48.5%; Pred. No. 0.00015;
tive 0; Mismatches 156; Indels 0;
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APPLICANT: HINUMA, Shuji
APPLICANT: YOSHIDA, Hiromi
APPLICANT: YOSHIDA, Hiromi
APPLICANT: HABATA, Yugo
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: Novel RFRP-3 And Its DNA
TITLE OF INVENTION: Novel RFRP-3 And Its DNA
TITLE REPERENCE: 2944USOP
CURRENT APPLICATION: NUMBER: US/11/223,294
CURRENT FILING DATE: 2006-09-09
PRIOR PELICATION NUMBER: US/10/487,634
PRIOR PELICATION NUMBER: PCT/JP02/08466
PRIOR PLING DATE: 2004-02-24
PRIOR PLING DATE: 2004-02-24
PRIOR PLING DATE: 2004-02-24
PRIOR PLING DATE: 2004-02-24
PRIOR PLING DATE: 2005-08-25
PRIOR APPLICATION NUMBER: UF/JP02/08466
PRIOR PLING DATE: 2005-08-25
NUMBER OF SEQ ID NOS: 78
                                                                                   Sequence 20, Application US/10473173
Publication No. US20060088823A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 38, Application US/11223294; Publication No. US20060035332A1
                                                                                                                                                                  APPLICANT: VAN ANDEL INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 147; Conservative
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TITLE OF INVENTION: A Method for Distinguishing Follicular Tyroid Adenoma (FTA) from
TITLE OF INVENTION: Pollicular Thyroid Carcinoma (FTC)
TITLE OF INVENTION: FOllicular Thyroid Carcinoma (FTC)
TITLE REPREBNCE: 000250.00021
CURRENT APPLICATION NUMBER: US/11/100,640
CURRENT FILING DATE: 2005-04-07
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 33
LENGTH: 1329
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                                                                                                                                                                          GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGT 314
                                                                                                                                                                                                                                                                                          315 GTTCACAGCGATTCCAGTCACACGTACGCGATGACCAAAGACTGGGCATTCGGGTC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                          375 AGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAG 434
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                                                                                              298 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 357
                                                                                                                                              GTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAACAAGCG 254
238 AAATCAITCAGICCACICIAAITICICAGAGAAGAAIGCCCAGCTICIGGCITITIGAAAA 297
                                             CGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCTTCTACGGGTTCCT 194
                                                                                                                                                                                                                                                                                                                                                                                          478 CATCATGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA
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48.5%; Pred. No. 0.00014;
tive 0; Mismatches 156; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 CCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.5
Matches 147; Conservative
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US-11-100-640-33
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                                                                                                                                                                                                                                                                                                                       CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 GGGCATGTCCGTGTCTGCATCGGTTTTCACACTGGCCATCGCTGCTGGAAAGGTTCCG 500
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Sequence 4059, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT APPLICATION NUMBER: US 60/5-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4059
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                                                                                                                                                                                  CGTACTATGGGCGGTGGCGAGAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT
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Pred. No. 0.004;
0; Mismatches 107; Indels
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Matches 113; Conservative (
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Publication No. US20050260687A1

GENERAL INFORMATION:

APPLICANT: Gerald, Christophe P.G.

APPLICANT: Bonini, James A.

APPLICANT: Browsky, Beth E.

APPLICANT: Craig, Douglas A.

TITLE OF INVENTION: And Uses Thereof

TITLE OF INVENTION: And Uses Thereof

TITLE OF INVENTION: And Uses Thereof

TITLE OF INVENTION: And Uses Thereof

TILLE OF INVENTION: And Uses Thereof

FILE REPERENCE: 57155-D/JVPW

CURRENT APPLICATION NUMBER: US/10/992,577

CURRENT APPLICATION NUMBER: US/09/538,036

FRIOR APPLICATION NUMBER: 09/405,558

FRIOR APPLICATION NUMBER: 09/405,558

FRIOR APPLICATION NUMBER: 09/405,558

FRIOR PRILING DATE: 1999-09-29

FRIOR PILING DATE: 1999-02-22

FRIOR FILING DATE: 1999-02-22

FRIOR FILING DATE: 1999-09-25

NUMBER OF SEQ ID NOS: 71

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4.2%; Score 50; DB 10; Length 1410;
Best Local Similarity 45.9%; Pred. No. 0.0014;
Matches 170; Conservative 0; Mismatches 200; Indels
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Pred. No. 0.0013;
0; Mismatches 200; Indels
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Best Local Similarity 45.9%;
Matches 170; Conservative
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                                                                  ; TYPE: DNA
; ORGANISM: Rat
US-11-223-294-38
SEQ ID NO 38
LENGTH: 1299
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Best Local Similarity
Matches 113; Conserv
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LENGTH: 3295
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Publication No. US20060084096A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOESS, FRANZISKA
APPLICANT: WOLF, DETLEF
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
TITLE OF ILLING DATE: 2005-09-12
CURRENT APPLICATION NUMBER: US/11/224,525
CURRENT APPLICATION NUMBER: 10/388,934
PRIOR APPLICATION NUMBER: EP 02005336.9
PRIOR APPLICATION NUMBER: EP 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR PILING DATE: 2002-03-14
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 594
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                                                                                                                                APPLICANT: BOESS, FRANZISKA
APPLICANT: BUTER-DICK, LAURA
APPLICANT: SUTER-DICK, LAURA
APPLICANT: WOLF, DETLER
TITLE OF INVENTION: BICHARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
FILE REFERENCE: 21199 US2
CURRENT APPLICATION NUMBER: US/11/224,663
CURRENT FILING DATE: 2005-09-12
PRIOR FILING DATE: 2005-09-12
PRIOR FILING DATE: 2005-09-14
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: Patentin version 3.1
SEQ ID NO 594
LENGTH: 3219
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4.1%; Score 48.8; DB 18; Length
Best Local Similarity 51.4%; Pred. No. 0.004;
Matches 113; Conservative 0; Mismatches 107; Indels
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                     Sequence 594, Application US/11224663
Publication No. US20060078921A1
GENERAL INFORMATION:
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US-11-224-525-594
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Query Match

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US-11-136-527-2750
US-11-136-527-2750
Sequence 2750, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Worth
APPLICANT: Wouth
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE OF INVENTION: 01896-041000 (AM101086)
FILE REPERENCE: 01896-041000 (AM101086)
CURRENT APPLICATION UNDER: US/11/136,527
CURRENT PILING DATE: 2005-05-25
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APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/5714,294

PRIOR FILING DATE: 2005-05-26
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4.1%; Score 48.8; DB 17; Length
Best Local Similarity 51.4%; Pred. No. 0.004;
Matches 113; Conservative 0; Mismatches 107; Indels
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Conservative 0; Mismatches 107; Indels
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SOFTWARE: PatentIn version 3.2
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US-11-136-527-3736
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395 IGGCAGTACAAGIGICCACAAIAACIIIGACAGICAIIGGCTIIGGACCGACAIC 448
                                                                                                                                                                                   Score 47.6; DB 17; Length 1147;
Pred. No. 0.0062;
0; Mismatches 154; Indels 0;
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin vergion 3.2
SEQ ID NO 2750
LENGTH: 1147
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Best Local Similarity 47.6%;
Matches 140; Conservative (
                                                                                                            ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2750
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Search completed: May 8, 2006, 14:58:45 Job time : 627 secs

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8, 2006, 14:31:48 ; Search time 255 Seconds (without alignments) 8316.200 Million cell updates/sec
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

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                                                                                              OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		مد			SUMMARIES		
KeBult No.	Score	Query	Query Match Length DB	DB	E C	Description	
7	1193	100.0	1193	e	US-09-721-870-104	Sequence 104, App	
7	1193	100.0	1500	٣	US-09-721-870-39	39,	
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80	61.6	5.2	1302	ო	US-09-255-368-5	5	
6	61.6	5.2	1302	ო	US-09-405-558-5	2	
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11	61.6	5.2	1903	m	US-09-719-088B-4	Sequence 4, Appli	
12	60.2	5.0	1803	m	US-09-693-746-1	٦,	
13	57.8	4.8	1605	m	US-09-676-970-1	,	
14	57.8	4.8	1605	m	US-09-676-972B-1	<u>-</u>	
15	57.8	4.8	1605	m	US-09-016-434-1231	123	
16	57.8	4.8	1605	٣	US-09-676-941A-1	ij	
11	57.8	4.8	1605	m	US-10-013-846-3	m	
18	57.8	4.8	1605	ო	US-10-291-446-1	7	
19	57.8	4.8	1605	ო	US-10-410-648-3	m	
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CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG

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Sequence 9, Appli Sequence 11, Appli Sequence 1, Appli Sequence 496, Appli Sequence 1203, Ap Sequence 1203, Ap Sequence 13, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli	RECEPTORS	Length 1193; Indels 0; Gaps 0; CAACGACTCCCTCCACCATC 60 CAACGACTCCTCCACCATC 60 CAACGACTCCTCCACCATC 120 ITCAGATCGCTGAGGCGATT 120 ITCAGATCACTTCACATT 120 ICCGATCAATCTTCACATT 120 ICCGATCAATCTTCACATTC 180 ICCGATCAATCTTCACATTC 180
US-09-721-870-9 US-09-721-870-11 US-09-045-186-1 US-09-045-186-3 US-09-045-186-3 US-09-016-434-1203 US-08-910-864-13 US-08-911-157-2 US-09-931-157-2 US-09-911-157-2 US-09-911-157-2 US-09-1130-3 US-09-1130-3 US-09-1130-3 US-09-119-08BB-5 US-09-119-08BB-5 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1 US-09-255-36B-1	GNMENTS PROTEIN-COUPLED 1,870 : CEGPCR19.2	Score 1193; DB 3; Pred. No. 0; O; Mismatches 0; Accarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarrrcancoarracarrac
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Query Match
Best Local Similarity 100.
Matches 1193, Conservative
                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (1)..(1497)
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Patent No. 6532621
APPLICANT: Lowery, David E. APPLICANT: Geary, Tinothy G. APPLICANT: Klaik, Tessa M. APPLICANT: Klaik, Tessa M. APPLICANT: Larsen, Martha J.
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CURRENT APPLICATION WINDER: U8/09/721,870
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55 1 ATGGTTAGTTCGGCGGCCACTTTCGACCATTTCAACCACAACGACT Indels 3, ö DB) OTHER INPORMATION: Clone identifier: CEGPCR19 US-09-721-870-39 100.0%; Score 1193; 100.0%; Pred. No. 0; 0; Mismatches 1027 721 967 요 ઠે 셤

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APPLICANT: Geary, Timothy G.
APPLICANT: Rubiak, Teresa M.
APPLICANT: Abiak, Teresa M.
APPLICANT: Abiak, Teresa M.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 28341/623
FILE REFERENCE: 28341/623
CURRENT APPLICATION NUMBER: US/09/721,870
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
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Patent No. 6632621
GENERAL INFORMATION:
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; Sequence 35, Application US/09721870; Patent No. 6632621
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ORGANISM: Homo sapiens
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US-09-721-870-35
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8.1%; Score 96.6; DB 3; Length 1130;
Best Local Similarity 47.0%; Pred. No. 1.3e-20;
Matches 438; Conservative 0; Mismatches 454; Indels 39; Gaps
                                                                                                                            APPLICANT: Lowery, David B.
APPLICANT: Lowery, Timothy G.
APPLICANT: Geary, Timothy G.
APPLICANT: Geary, Timothy G.
APPLICANT: Mublak, Tersea M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS FILE REPREMENCE: 28341/6223
CURRENT APPLICATION NUMBER: US/09/721,870
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 1130
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US-09-721-870-21
                               Sequence 21, Application US/09721870 Patent No. 6632621 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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FEATURE:
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                                                                                                 CACAAAAGCAGAGAAGTGATGCGACGTCACGA
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APPLICANT: Lowery, David B.
APPLICANT: Geary, Timothy G.
APPLICANT: Geary, Timothy G.
APPLICANT: Malasen, Martha J.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 28341/6228.
CURRENT APPLICATION NUMBER: US/09/721,870
CURRENT FILING DATE: 2000-11-24
NUMBER: OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
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50.5%; Pred. No. 1.6e-16;
tive 0; Mismatches 200; Indels
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734 ATTGCTACTTCAAAATCTTGCAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAAT 793
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Pred. No. 8.9e-11;
0; Mismatches 199;
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US-09-721-870-25
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Best Local Similarity 48.3%;
Matches 186; Conservative
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FEATURE:
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                     467 ATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTC 526
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6.6%; Score 78.8; DB 3; Length 1352;
Best Local Similarity 47.4%; Pred. No. 9.2e-15;
Matches 381; Conservative 0; Mismatches 402; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lowery, David B.
APPLICANT: Geary, Timothy G.
APPLICANT: Rubiak, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OP INVENTION: MoDULATORS OF G PROTEIN-COUPLED RECEPTORS FILE REPERENCE: 28141/6223
CURRENT APPLICATION NUMBER: US/09/721,870
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                      TTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570
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Sequence 15, Application US/09721870
Patent No. 6632621
GENERAL INFORMATION:
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LOCATION: (1)..(1350)
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Patent No. 6262246

GENERAL INFORMATION:

APPLICANT: Gerald, Christophe P.G.

APPLICANT: Bonini, James A.

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                                                                                                                                                                        CTCAACACTGATAAATCTACCGTAT
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RESULT 9 US-09-405-558-5

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APPLICANT: Gerald, Christophe P.G.
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Jones, Kenneth A.
APPLICANT: Jones, Kenneth A.
APPLICANT: Bonini, James A.
APPLICANT: Borini, James A.
APPLICANT: Browney, Beth E.
APPLICANT: Craig, Douglas A.
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
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TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
FILE REPERENCE: 57155-C
CURRENT APPLICATION NUMBER: US/09/141,113
EARLIER PELING DATE: 1999-09-24
EARLIER PELING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.0 - beta
FRACIER PLANCE
FRACIER PATENTION NUMBER: DATE: 1999-02-52
SEQ ID NOS: 71
FRACIER PATENTION NUMBER: DATE: 1999-02-52
FRACIER PATENTION NUMBER: DATE: 1999-03-62
SEQ ID NOS: 71
FRACIER PATENTION NUMBER: DATE: 1999-03-62
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Patent No. 6849727

GENERAL INFORMATION:
APPLICANT: Geral, Kenneth A.
APPLICANT: Borousky, Beth B.
APPLICANT: Craig, Douglas A.
TITLE OF INVENTION: DNA REcoding Mammalian Neuropeptide FF (NPFF) Receptors
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Pred. No. 3.7e-09;
0; Mismatches 234; Indels
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Best Local Similarity 46.3%;
Matches 202; Conservative (
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Patent No. 6709831
GENERAL INFORMATION:
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512 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 571
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                                                                                           5.2%; Score 61.6; DB 3; Length 19
46.3%; Pred. No. 4.7e-09;
ive 0; Mismatches 234; Indels
  ; TYPE: DNA; CRGANISM: Homo sapiens NPY-Y7-encoding gene US-09-719-088B-4
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CURRENT FILING DATE: 2000-10-20
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PRIOR FILING DATE: 1999-10-22
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US-09-693-746-1
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SOFTWARE: PatentIn version
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Pred. No. 3.7e-09;
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GREKEAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 12020-0003; CURRENT PAPLICATION NUMBER: US/09/719,08BB; CURRENT PILING DATE: 2000-12-08; PRIOR APPLICATION NUMBER: PCT/AU99/00523; PRIOR APPLICATION NUMBER: AU PP4385; PRIOR APPLICATION NUMBER: AU PP4385; NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 4; LENGTH: 1903
              FILE REPERENCE: 57155-D/JPW
CURRENT APPLICATION NUMBER: US/09/538,036
CURRENT FILING DATE: 2000-03-29
FEARLIER APPLICATION NUMBER: 09/405,558
EARLIER PILING DATE: 1999-09-24
EARLIER PILING DATE: 1999-02-22
EARLIER FILING DATE: 1999-02-22
EARLIER FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 5
INVENTION: And Uses Thereof
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Matches 202; Conservative
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; ORGANISM: Homo sapiens
US-09-538-036-5
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Sequence 1, Application US/09693746
Patent No. 6835546
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lowery, David B.
APPLICANT: Smith, Valdin G.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Larsen, Marcha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And MethorITLE OF INVENTION: Related To The Same
FILE REFERENCE: 629.1cp
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APPLICANT: Darrow, James W.
APPLICANT: Darrow, James W.
APPLICANT: De Lombaert, Stephane
APPLICANT: De Lombaert, Stephane
APPLICANT: Tran, Jennifer
APPLICANT: Tran, Jennifer
APPLICANT: Tran, Jennifer
APPLICANT: Carpino, Philip Albert
TITLE OF INVENTION: Amino Substituted Pyrazolo [1,5,-a]-1,5-Pyrimidines and
TITLE OF INVENTION: Pyrazolo [1,5-a]-1,3,5-Triazines
FILE REPERENCE: U 012956-1
CURRENT APPLICATION NUMBER: US/09/676,972B
CURRENT PILING DATE: 200-09-29
PRIOR FILLING DATE: 1999-09-30
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                                                  315 GTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGGCATTCGGGTC
                                                                                                                                              375 AGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGGTGTTTGTGACGAGTTGGAG
                                                                                               CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTTGGTGA
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Pred. No. 7.3e-08;
0; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/09676972B; Patent No. 6476038
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Best Local Similarity 46.44
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-676-972B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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          191 TCCTGTTTGTATTAGGCATTTTTGGAAACGGCGCGTACTATGGGCGGGGGGGAGAACA 250
                                        251 AGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATAT 310
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APPLICANT: Blum, Charles
APPLICANT: Tarn, Jennifer
APPLICANT: Tran, Jennifer
APPLICANT: Gianglordano, Mark
APPLICANT: Grapino, Philip Albert
ITLE OF INVENTION: Certain Alkylene Diamine-Substituted Pyrazolo
ITLE OP INVENTION: [1,5,-a]-1,5-Pyrimidines and pyrazolo
ITLE OP INVENTION: [1,5,-a]-1,5-Pyrimidines
FILE REPRENCE: U012955-3
CURRENT APPLICATION NUMBER: 105/09/676,970
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 1
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4.8%; Score 57.8; DB 3; 1
Best Local Similarity 46.4%; Pred. No. 7.3e-08;
Matches 188; Conservative 0; Mismatches 217;
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Patent No. 6372743
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De Lombaert, Stephane
Blum, Charles
Tran, Jennifer
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APPLICANT: Darrow.
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LENGTH: 1605
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226 AAATCATTCAGTCCACTCTAATTTCTCAGAGAAGAATGCCCAGCTTCTGGCTTTTGAAAA 285
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                                         Sequence 1231, Application US/09016434

Batent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION POR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PAHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STATE: JA14 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: NOR PEFFECT 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: WOS OF WASHER:
FILING DATE: HEREWITH
FILING DATE: HEREWITH
FILING DATE: HEREWITH
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tive 0; Mismatches 217; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELLING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REGISTRATION NUMBER: 37,071

REPERBURE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1231:

SEQUENCE CHARACTERISTICS:

LENGTH: 1605 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

INMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9189155

US-09-016-434-1231
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Best Local Similarity 46.41
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: HE
RESULT 15
US-09-016-434-1231
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OY 375 AGTGATGACCATTTAGTTCCTTTGTCAAATTCGTGTTTGTGACGAGTTGGAG 434

Db 526 GGCGATGTGAATCCTTTGTGCAATGGTTTCAATCGTGTCCATTTTCTC 585

QY 435 CCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479

Db 586 TCTGGTTCTCATTGGATAAATTCTGCATATCAACGATCC 630
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Search completed: May 8, 2006, 14:48:09 Job time : 257 secs



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8, 2006, 09:29:53; Search time 41 Seconds (without alignments) 931.660 Million cell updates/sec
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                         OM protein - protein search, using sw model
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US-10-650-467-105 2074 1 MVSSAATISTITTPSTI......QLHDLLPTSTHSDRCAGNSF 397 Title: Perfect score: Sequence:

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 2 T19340 hypothetical protein C16D6.2 - Caenorhabditis elegans

somatostatin recep somatostatin recep bombesin receptor, somatostatin recep

somatostatin recep allatostatin recep	Phel3 bombesin rec	hypothetical prote hypothetical prote	somatostatin recep	tachykinin recepto	galanin receptor 1	neurokinin 2 recep	neurokinin 3 recep	somatostatin recep	kappa-type opioid	brain-specific som	somatostatin recep	galanin receptor -
A41795 JC7677	150102	T15622 T32517	B41795	\$17783	159336	S20303	S55524	S29248	A44081	A47249	JN0605	JC7209
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284.5	283.5	282.5	281.5	281	280.5	279.5	279.5	278	277.5	276.5	276.5	276.5
30	35	ы ы ы 4	32	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT T27559 Dypoth C, Spec. C, Dace C, Acce R, Ains Bubmitt A, Refer A, Refer A, Rele A, Rele A, Rele A, Rele	RESULT 1 T27559 hypothetical protein ZC412.1 - Caenorhabditis elegans hypothetical protein ZC412.1 - Caenorhabditis elegans C;beciese Caenorhabditis elegans C;bate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004 C;Accession: T27559 R;Ainscough, R. Ribmitted to the EMBL Data Library, August 1996 A;Accession: T27559 A;Accession: T27559 A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-539 < WIL- A;Ccss:_references: UNIPRCT:Q23305; UNIPARC:UPI0000083344; EMBL:Z78067; PIDN:CAB01528.1
A, Experimen C, Genetics: A, Gene: CES A, Map posit A, Introns:	A;Experimental source: clone ZC412 A;Gene: CESP:ZC412.1 A;Map position: 5 A;Introns: 29/3; 75/3; 112/1; 144/3; 180/3; 223/3; 241/3; 324/3; 376/2; 426/2; 456/3
Quer Best Matc	Query Match 29.3%; Score 607.5; DB 2; Length 539; Best Local Similarity 35.3%; Pred. No. 7.6e-44; Matches 119; Conservative 76; Mismatches 111; Indels 31; Gaps 7;
È	33 CIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV 92
đ	9 CIDVNAILQQFNDWTVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI 65
ò	93 FILNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVWCHLVPLSNSGSVFVTSWSLTAISLD 152
名	66 PLINLAVSDĽLCITAVPITPVLAFMKRMIFGIIMCKLVPTCQAFSVLISSMSLCYIAID 125
ò	153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGBT 206
셤	126 RYRSİVTPLREPMSDRHARMLLMPTMVVAFLASYPLYYSQNLKİMVIENV 175
È	207 PYCGHPCDBANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265
QQ	176 TLCGDFCGEFNWQSDEISKLTYTTSLLIIQLIIPAIIMSFCYLMILQKVQTDWLVDEGSM 235
ò	266 CQSLTQKQRSDATSRKKKVNYILJAMVVTFIGCWLPLTLLNLVKDFKKEPEW 317
д	236LTAAQQAQTAVRKRRVWYVLILMVIVFMACWFPLSAVNLFRDLGMRFFFCQTVYKVL 292
ò	318 LKROPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRS 354
q	293 MADQMYFKLLNVHVIAMTSIVWNPVLYFWMSKRHRRA 329

us-10-650-467-105.rpr

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A;Cross-references: UNIPROT:09XXU4; UNIPARC:UPI000003C148; EMBL:AL008868; PIDN:CAA15513.
A;Experimental source: clone C53C7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 FTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM 117
                                                                                                                                                                                                                                    237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 VPFAVMAPCYANIVSVLSKRAQTKIRKMVERTSALESSCAPPSHGLEQYENELNEFLDKQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----WAIN--AHVIAMSLVVWNPLLPFWL-----TRKOKRSGLSKILNST---- 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 DYDISYLLMLFTHSIAMSNNVLNPVLYAMLNPSFROLVIKTYFGDRRKSDRIINQTSVYK 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 NAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apported to protein C53C7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20184
R;Mortimore, B.
R;Mortimore, B.
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R;Mortimore, B.
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R;Mortimore, B.
R;Molecule type: Call Data Library, November 1997
R;Status: preliminary; translated from GB/EMBL/DDBJ
R;Status: preliminary; translated from GB/EMBL/DDBJ
R;Status: DNA
R;Residues: 1-365
R;Mills
R;Residues: 1-365
R;Mills
R;Residues: 1-365
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                                                                                                                                                                                            118 TKDWAPGSVMCHLVPLSNSCSVPVTSWSLTAISLDKPLHINDPTKQPVSIRQALAITFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 VPMAVITYCYFKILQKVSK-----DMIIQNA------QPCQSLT----
                                                                                                         29 FLITVYLFLPFIGLFGNVTLIYVTCSHKALLSVQNIFILNLAASDCMMCILSLPITPITNV
                                                                                                                                                                                                                                                                                                                          WIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHPCDRANWQSENSRKIYGTTVMLLQFV
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         77; Gaps
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         Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: X
A;Introns: 40/2; 108/3; 136/2; 193/1; 254/3; 298/2; 336/3
C;Superfamily: neurokinin 1 receptor
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         69
         Conservative
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         Matches 117;
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C;Species: Caenorhabditis elegans
C;Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19340
A;Gardher, A.
A;Reference number: Z19111
A;Accession: T19340
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A;Accession: T1934
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A;Accession: T1934
A;Accession: CBSP: C1606.2
A;Accession: Z3/3; S6/2; 107/3; 147/3; 267/2; 306/3
C;Superfamily: neurokinin 1 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 ARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VPNLFILSLSCSDIVVCCTSATITFITAFKKEWIFGEALCRIAPFIAGISLCFSTFTLTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLIQKORSD------AISRKKKVNYILIAMVVIPIGCWLPLILLNLVKDFKKEP 315
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| Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
| Accession: T29741
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---KKQKIDNWEMELSDQQRIAVKRQRINRMLIGMVVAFACSWIWSVTFNILRDYSYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EWLKROPFFWAINAHVIAMSLVVWNPLLF-------FWLTRKOKRSG--LS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 24.8%; Score 514; DB 2; Length 37 sal Similarity 31.3%; Pred. No. 4.5e-36; 114; Conservative 74; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C39E6.6 - Caenorhabditis elegans C;Species: Ceenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_oC;Accession: T29741
R;Pulton, B.; Le, T.
submitted to the EMBL Data Library, February 1996
A;Pescription: The sequence of C. elegans cosmid C39E6.
A;Reference number: Z20676
A;Recession: T29741
A;Residua: preliminary; translated from GB/EMBL/DDBJ
A;Mesidua: preliminary;
A;Residua: 1-457 <FUL>
A;Residua: 1-457 <FUL>
C;Genetics:
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Best Local Similarity
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A;Introns: 58/3; 107/
C;Superfamily: neurok
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Matches
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A;Cross-references: UNIPROT:P90745; UNIPARC:UPI000003C14C; EMBL:Z83217; PIDN:CAB05681.1 A;Experimental source: clone C10C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 DITVDPYIRSIPTFLYGFLFVLGIFGNGGVLMAVARNKRLQSARNVFLLNLIFTDLILVF 106
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNL--VKDFKKEPEWLKRQ 321
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                                                                                                                                                                                                                                                                                ; Score 387.5; DB 2; Length 373; ; Pred. No. 2.6e-25; 69; Mismatches 98; Indels 35
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18.4%; Score 382; DB 2; Length 376
Best Local Similarity 28.7%; Pred. No. 7.8e-25;
Matches 92; Conservative 78; Mismatches 127; Indels
                C;Genetics:
A;Gene: CESP:T05Al.1
A;Map position: 4
A;Introns: 48/2; 106/3; 219/2; 254/1; 280/1; 309/1; 327/2
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A;Accession: T19186
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 54/3; 105/3; 133/3; 179/2; 251/2; 348/3
C;Superfamily: neurokinin 1 receptor
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                                                                                                                                                                                                                                                                                           18.7%;
                                                                                                                                                                                                                                                                                                                                                                                         89; Conservative
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Best Local Similarity
Matches 89; Conserv
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T24487
R;Lloyd, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19897
A;Reference number: Z19897
A;Accession: T24487
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A;Accession: T23487
A;Accession: T23487
A;Accession: T25884
A;Accession: T25884
A;Residues: L373 <WLL>
A;Coss-references: UNIPROT:Q22188; UNIPARC:UPI00001641C3; EMBL:Z68219; PIDN:CAA92481.1;
A;Experimental source: clone T05Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F41E7.3 - Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
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CjSpecies: Caenorhabditis elegans
CjSpecies: T2076
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227 GSQ--KELMSEARRQLTQRRLRTWRMLIIMTVTFALSWLPSVGFNFLRDYSALFGIIDSQ 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 CSVFVTSWSLTAISLDKP-----LHINDPTKQPVSIROALAITFLIWIVSTLINLP 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 TYCYFKILQKVSKDMIIQNAQPCQSLIQKQRSDATSRKKKNNYILLIAMVVTFIGCWLPLT 303
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                                                                                                                                                                                                                        322 PFFWAINAHVIAMSLVVWNPLLPFWLTRKQKRSGLSKILNSTEGSKKAGGSGLRGI 377
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A;Introns: 76/2; 161/3; 220/3; 279/2; 325/2; 350/1; 378/1
C;Superfamily: neurokinin 1 receptor
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Best Local Similarity 29.4%; Pred. No. 5.6e-28;
Matches 101; Conservative 72; Mismatches 94
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A; Residues: 1-384 <-HRR>
A; Residues: 1-384 <-HRR>
A; Cross-references: UNIPROT: P25929; UNIPARC: UDIO0002D509; GB: L07615; NID: g189284; PIDN: A; Cross-references: UNIPROT: P26929; UNIPARC: UDIO0002D509; GB: L07615; NID: g189284; PIDN: A; Otcos: sequence extracted from NCB1 backbone (NCBIN: 128005, NCBIP: 128000)
R; Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A; Title: Cloned human neuropeptide Y receptor couples to two different second messenger A; Reference number: A46133; MUID: 92335184; PMID: 1321422
A; Accession: A46133
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-384 <-HEZ>
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A;Cross-references: UNIPARC:UP1000002D509
A;Note: sequence extracted from NCB1 backbone (NCBIP:108538)
B;Note: sequence extracted from NCB1 backbone (NCBIP:108538)
J; Biol. Chem. 267, 10935-10938, 1992
J; Biol. Chem. 267, 10935-10938, 1992
A;Fitle: Cloning and functional expression of a human neuropeptide Y/peptide YY receptor A;Reference number: A42773; MUID:92283782; PMID:1317848
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Sibperfamily: neurokini I receptor
C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
F;37-66/Domain: transmembrane #status predicted <TM1>
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C;Species: Hower spices (man)
C;Accession: A55490; A46133; A42773
C;Accession: A55490; A46133; A22773
R;Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
J. Biol. Chem. 268, 6703-6707, 1993
A;Title: Genomic organization, localization, and allelic differences in the gene A;Reference number: A45490; MUID:93203272; PMID:8095935
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A;Note: seguence extracted from NCBI backbone (NCBIN:104735, NCBIP:104736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 LTCHCRSPQGES-----EHLPLSTVHTDLSKGS 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuropeptide Y/peptide YY receptor Y1 - human
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A;Molecule type: mRNA
A;Residues: 1-384 <LAR>
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C;8pecies: Mus musculus (house mouse)
C;8pecies: Would 1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: 863685
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                                                                                                                                                                                                                                                             RESULT 8

I 52315
G protein-coupled receptor UHR-1 - rat
C; Species: Rattus sp. (rat)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
C; Accession: 152315
R; Welch, S. K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.
Biochem. Biophys. Res. Commun. 209, 606-613, 1995
A; Title: Sequence and tissue distribution of a candidate G-coupled receptor clon A, Reference number: 152315, MUID:95251659; PMID:7733930
A; Accession: 152315
A; Attus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-370 < RES
A; Cross-references: UNIPARC:UP1000004B9B3; GB:S77867; NID:g998527; PIDN:AAB34129
C; Superfamily: neurokinin 1 receptor
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252 MMIVMVVGFVLAMMPFNAVNLYRDLFGISKWYST---VFAL-CHVCAMCSAVLNPIIYSW 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ENNRVVPGSVTGSQADMDRARRRTFCLLVVVVVVPALCMLPLHIFNLLRDL--DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 STISNVITSHSNNGSCIQIARAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAIDPYAFGLVQLLCHWLAMSSACYNPFIYAWL-HDSFREELRKMLLS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.0%; Score 373.5; DB 1 26.7%; Pred. No. 4.1e-24;
                                                                               347 LTRKOKRSGLSKILNSTEGSK 367
                                                                                                                                                      308 F-NPOFROSITTLFKGTDEAR 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 26.71
Matches 93, Conservative
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neuropeptide Y receptor - fruit fly (Drosophila melanogaster)
NiAlternate names: G protein-coupled receptor PR4
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A41738
R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.
J. Biol. Chem. 267, 9-12, 1992
A;Ittle: Cloning, functional expression, and developmental regulation of a neuropeptide A;Reference number: A41738; MUID:92112730; PMID:1370455
A;Accession: A41738
A;Molecule type: mRNA
A;Residues: 1-449 <LIA>
A;Conetics:
C;Genetics:
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: $12863; $19101
R;Eva, C.; Keinaenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.
FEBS Lett. 271, 81-84, 1990
FFBS Lett. 271, 81-84, 1990
A;Fitle: Molecular cloning of a novel G protein-coupled receptor that may belong to the A;Reference number: $12863; MUID:91032093; PMID:2172008
                  254 VSKOMIIQNAQFCQSLTQKQRSDATSRKKKVNYILLIAMVVTFIGCWLPLTLLNLVKOFKK 313
                                                                                                                                                                                                    223 SRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMILQNAQFCQSLTQKQRSDATSRKK 282
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C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein
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6.5e-21;
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                                                                                                                                                                                                                                                                                                                    314 EPEWLKROPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKR 353
                                                                                                                                                                                                                                                                                                                                                                                OINTCHMNLLFLL-CHLTAMISTCVNPIFYGFLNKNFQR
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C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S27388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 PPONVTLDAYKOK-----YVCFD-OFPSDSHRLSYTTLLLVLQYFGFLCFIFICYFKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 384;
                       File-136/Domain: transmembrane #status predicted <TW3>
File-179/Domain: transmembrane #status predicted <TW3>
File-179/Domain: transmembrane #status predicted <TW4>
Fig.09-232/Domain: transmembrane #status predicted <TW6>
Fig.03-232/Domain: transmembrane #status predicted <TW6>
File-198/Domain: transmembrane #status predicted <TW6>
Fill-198/Disulfide bonds: #status predicted <TW7>
Fill3-198/Disulfide bonds: #status predicted <TW7>
File-198/Binding site: carbohydrate (Asn) (covalent) #status predicted File-186/Binding site: palmitate (Cys) (covalent) #status predicted
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16.5%; Score 342; DB 2; Length 382;
1 Similarity 25.6%; Pred. No. 2e-21;
87; Conservative 80; Mismatches 155; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             16.7%; Score 346.5; DB 2;
25.7%; Pred. No. 8.4e-22;
iive 78; Mismatches 154;
F;77-103/Domain: transmembrane #status predicted
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Conservative 7
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Best Local Similarity
Matches 87; Conserv
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Matches 88; Conserv
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A,Reference number: 139163; MUID: 96032678; PMID: 7559383
A,Accession: 139163
A,Accession: 139163
A,Accession: 139163
A,Accession: 139163
A,Minimary; translated from GB/EMBL/DDBJ
A,Residues: Preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-133, 'A', 135-381 <ROS>
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A,Reference number: H01019
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A; Map position: 4g31-4g31
C; Superfamily: neurokinin 1 receptor
C; Superfamily: neurokinin 1 receptor
C; Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
C; Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
F; 49-76/Domain: transmembrane #status predicted <TM1>
F; 87-113/Domain: transmembrane #status predicted <TM5>
F; 216-138/Domain: transmembrane #status predicted <TM6>
F; 21-237/Domain: transmembrane #status predicted <TM6>
F; 21-237/Domain: transmembrane #status predicted <TM6>
F; 21-23/Domain: transmembrane #status predicted <TM6>
F; 21-23/Domain: transmembrane #status predicted <TM6>
F; 21-23/Domain: transmembrane #status predicted <TM6>
F; 21-23/Domain: transmembrane #status predicted <TM7>
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Cispecies: Homo sapiens (man)
Cispecies: UnMar-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
Cispecs on: 139187; 139163; G02301
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A;Cross-references: UNIPARC:UP1000016818D; EMBL:U42389; NID:91314329; PIDN:AAB07760.1;
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                                                                         18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL
    Gaps
    18;
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81; Mismatches 155;
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A,Molecule type: mRNA
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        Conservative
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A; Residues: 1-381 <GER>
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        96;
        Matches
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A; Reference number: 819101
A; Reference number: 819101
A; Reference number: 819101
A; Rolecule type: mRNA
A; Residues: 1-343, 'DDYETIAMSTMHTDVSKTSLKQASPVAFKKISMNDNBKI' <KRA>
A; Residues: 1-343, 'DDYETIAMSTMHTDVSKTSLKQASPVAFKKISMNDNBKI' <KRA>
A; Residues: 1-343, 'DDYETIAMSTMHTDVSKTSLKQASPVAFKKISMNDNBKI' <KRA>
A; Residues: 1-343, 'DDYETIAMSTMHTDVSKTSLKQASPVAFKKISMNDNBKI' <KRA>
A; Residues: 1-343, 'DDYETIAMSTMHTDVSKTSLKQASPVAFKKISMNDNBKI' <KRA>
A; Residues: 1-343, 'DDYETIAMSTMHTDVSKTSLKQASPVAFKKISMNDNBKI' <KRA>
C; KSAPVORGS: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TMI>
F; 39-61/Domain: transmembrane #status predicted <TMI>
F; 114-135/Domain: transmembrane #status predicted <TMI>
F; 213-21/Domain: transmembrane #status predicted <TMI>
F; 26-285/Domain: transmembrane #status predicted <TMF>
F; 26-285/Domain: transmembrane #status predicted <TMF>
F; 29-322/Domain: transmembrane #status predicted <TMF>
F; 28-11, 17/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 346/Binding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cipate: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
Cipate: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
Cipate: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
Cipate: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
Riberacy H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A; Reference human neuropeptide Y receptor couples to two different second messenger
A; Reference number: A46133; MUID:92335184; PMID:1321422
A; Accession: B46133
A; MulD:92335184; PMID:1321422
A; Accession: Defaultary; not compared with conceptual translation
A; Residues: 1-382 <HER>
A; Residues: 1-382 <HER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 IIILKQKEMRNVTNILIVNLSFSDLLVAVMCLPPTFVYTLMDHWVFGETMCKLNPFVQCV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVPVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 SFYVQPGETPYCGHFCDE----ANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQK 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 VSKDMIIQNAQPCQSLTQKQRSDATSRKKKVNYILLAMVVTFIGCWLPLTLLNLVKDFKK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 LKR----RNNHMDKIRDSKYRSSET---KRINVMLLSIVVARAVCWLPLTIFNTVFDWNH 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 STISNVITSHSNNGSCIQIARAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuropeptide Y/peptide YY receptor Y1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-Sep.1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C/Accession: B46133
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        A,Molecule type: mRNA
A,Residues: 1-349 <EVA>
A,Residues: 1-349 <EVA>
A)Cross-references: UNIPARC:UPI0000176632; EMBL:211504
A)Cross-references: UNIPARC:UPI0000176632; EMBL:211504
R,Krause, J.; Eva, C.; Beeburg, P.; Sprengel, R.
submitted to the EMBL Data Library, November 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch
1 Similarity 25.3%; Pred. No. 1.16-20;
86; Conservative 81; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 QIIATCNHNLLFLL-CHLTAMISTCVNPIFYGFLNKNFQR 328
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Pred. No. 1.2e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.1%;
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Best Local Similarity
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Matches 86; Conserv
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9
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                                                                                                                                                                                                                                     131 VPLSNSCSVFVTSWSLTAISLDKPLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM 190
                                                                                                                                                                                                                                                                                                            191 SFEH----VDGSFYVQPGETPYCGHPCDEANWQSENSRKIYGT----TVMLLQFVVPMAV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                      243 ITYCYFKILQKVSKDMI--IQNAQFCQSLTQKQRSDATSRKKKVNYILLIAMVVTFIGCWL 300
                                                                                                                                                                                                                                                                                                                                                                                       186 PREYSLIEIIPDFEIVA------CTE-KWPGB-EKSIYGTVYSLSSLLILYVLPLGI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 AEAIAAGGIDDITVDFY------IRSIFTFLYGFLFVLGI 70
                                                                                                                                                          301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRSGLS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 PLHAPQLAVDIDSQVLDLKEYKLIFTV-FHIIAMCSTFANPLLYGWMNSNYRKAFLS 338
                                                       Query Match 15.6%; Score 324; DB 2; Length 381;
Best Local Similarity 25.5%; Pred. No. 6.9e-20;
Matches 91; Conservative 67; Mismatches 139; Indels 60; Gaps
F;342/Binding site: palmitate (CyB) (covalent) #status predicted F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Search completed: May 8, 2006, 09:34:15 Job time : 42 secs THIS PAGE BLANK (USPTO)

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8, 2006, 09:26:17; Search time 187 Seconds (without alignments) 932.799 Million cell updates/sec
                                                                                                                                                                                                                     1 MVSSAATISTISTTTTPSTI.....QLHDLLPTSTHSDRCAGNSF 397
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Perfect
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result		Query				
No.	Score	Match	Length	80	QI	Description
1	2074	100.0	397	4	AAU03851	Aau03851 G protein
7	2074	100.0	499	4	AAU03820	Aau03820 G protein
m	1899	91.6	433	4	AAU03852	O
4	607.5	29.3	450	4	AAU03809	Aau03809 G protein
S	607.5	29.3	539	œ	ADN23955	ВВ
9	529	25.5	518	4	AAB86955	Aab86955 D. melano
7	529	25.5	900	4	ABB71560	Abb71560 Drosophil
80	529	25.5	909	4	AAU03205	Aau03205 Fruit fly
σ	529	25.5	900	7	AAE38182	Aae38182 Fruit fly
10	529	25.5	9	7	ADL83372	Ad183372 Drosophil
11	529	25.5	009	æ	ADR03092	N
12	529	25.5	9	6	ADV91972	_
13	521	25.1	009	7	ADE14524	Adel4524 Fruit fly
14	515.5	24.9	376	4	AAU03811	Aau03811 G protein
15	514	24.8	374	æ	ADN24291	_
16	485.5	23.4	457	4	AAU03813	Aau03813 G protein
17	485.5	23.4	457	œ	ADN24116	Adn24116 Bacterial
18	461.5	22.3	365	4	AAU03818	Aau03818 G protein
19	461.5	22.3	365	œ	ADN24305	Adn24305 Bacterial
20	460.5	22.2	387	4	AAU03808	Aau03808 G protein
21	458	22.1	381	4	AAU03807	Aau03807 G protein
22	458	22.1	402	4	AAU03805	Aau03805 G protein
23	458	22.1	404	4	AAU03804	Aau03804 G protein

The sequence represents a G protein-coupled receptor-like (GPCR-like) receptor protein. GPCR-like receptors and their associated nucleic acids may be used to identify candidate compounds for their ability to modulate the activity of GPCRs. The sequences therefore are useful for treating and preventing infection by endoparasitic and ectoparasitic invertebrate parasities, especially helminths and insects, and particularly ailments related to aberrant neurological and neuromuscular function

Sequence 397 AA;

Aau03806 G protein

4 AAU03806

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Claim 6; Page 175-176; 219pp; English.

Adn24230 Bacterial	Abg73520 D. rerio	04	Adl83376 Drosophil	Adr03096 Drosophil	Adv91976 DmGPCR2b,	Adn23444 Bacterial	Ado29366 Mouse GPC	Aaw27510 Consensus	Aar91218 Human pit	Aaw31379 Human G p	Aaw95181 Human G-p	Aaw97221 Human pit	Human	Abp81880 Human G p	Ado29365 Human GPC	Adt98602 Human wil	Aay87503 Murine G	Aab67653 Amino aci	Aay87505 Human G c	Aau03822 G protein
ADN24230	ABG73520	AAU03207	ADL83376	ADR03096	ADV91976	ADN23444	AD029366	AAW27510	AAR91218	AAW31379	AAW95181	AAW97221	AAG62539	ABP81880	AD029365	ADT98602	AAY87503	AAB67653	AAY87505	AAU03822
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412	375	458	458	458	458	373	370	380	370	370	370	370	370	370	370	370	370	370	370	376
20.2	18.8	18.7	18.7	18.7	18.7	18.7	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.4	18.4
419.5	390.5	388	388	388	388	387.5	386.5	386.5	386	386	386	386	386	386	386	386	385.5	385.5	382	382
25	26	27	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

G protein-coupled receptor-like receptor; GPCR-like receptor; helminth; endoparasite; ectoparasite; invertebrate; insect; neurological disorder; neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech; Using G-protein-coupled receptor (GPCR)-like receptors to identify candidate compounds for the treatment and prevention of invertebrate parasites, especially helminths and insects. G protein-coupled receptor-like (GPCR-like) receptor protein #23. Larsen MJ; AAU03851 standard; protein; 397 AA. Geary TG, Kubiak TM, 24-NOV-2000; 2000WO-US032225. 99US-0167523P. (PHAA) PHARMACIA & UPJOHN. (first entry) WPI; 2001-343952/36. N-PSDB; AAS07253. WO200138533-A2. Homo sapiens. 24-NOV-1999; 12-SEP-2001 31-MAY-2001. Lowery DE, AAU03851; fruitfly. RESULT 1 AAU0385; ô

Gaps

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120 222 180 282

342 300 402

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receptor protein. GPCR-like receptors and their associated nucleic acids may be used to identify candidate compounds for their ability to modulate the activity of GPCRs. The sequences therefore are useful for treating and preventing infection by endoparasitic and ectoparasitic invertebrate parasities, especially helmininhs and insects, and particularly ailments related to aberrant neurological and neuromuscular function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLTLINLVKDFKKEPEMLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRSGLSKIL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
                                                                                                                                                                                                                                                                                                                                                                                                        163 LYGFLEVLGIFGNGGVLMAVARNKRLQSARNVFLINLIFTDLILVFTALPVTEWYAMTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STLINIPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLTLIALVKOPKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL
                                                                                                                                                                                                                                                                                                                         MVSSAATISTISTITTPSTISNVITSHSNNGSCIQIABALAAQGIDDITVDFYIRSIFTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #AFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAIFFLMIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVITYCYPKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL
                                                                                                                                                                                                                                                                                                                                                                                     LYGPLFVLGI FGNGGVLWAVARNKRLQSARNVFLLNLI FTDLILVFTAI PVTPWYAMTKD
                                                                                                                                                                                                                                                                                              1 MVSSAATISTISTITTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-coupled receptor-like (GPCR-like) receptor protein #24.
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                                                                                                                                                                                                      100.0%; Score 2074; DB 4; Length 499; 100.0%; Pred. No. 6.2e-209; ive 0; Mismatches 0; Indels 0
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Matches 397; Conservative
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N-PSDB; AAS07254.
                                                                                                                                                                 Sequence 499 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2001
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                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVITYCYFKILQKVSKDMIIQNAQPCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL
                                                                                                                                                                                                                                         STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM
                                                                                                                                                               MVSSAATISTISTITTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF
                                                                                                                                                                                                             LYGFLFVLGI FGNGGVLWAVARNKRLQSARNVFLLNLI FTDLI LVFTAI PVTPWYAMTKD
                                                                                                                                                                                                                                                                                                    WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV
                                                                                                                                                                                                                                                                                                                                                                                          STLINLPYLMSPEHVDGSPYVQPGETPYCGHPCDEANWQSENSRKIYGTTVMLLQPVVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVITYCYPKILQKVSKDMIIQNAQPCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL
                                                                                                                       MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Using G-protein-coupled receptor (GPCR)-like receptors to identify candidate compounds for the treatment and prevention of invertebrate parasites, especially helminths and insects.
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-coupled receptor-like (GPCR-like) receptor protein #19.
                                                                            ö
                                  Length 397;
                                                                       Indels
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                             Score 2074; DB 4;
Fred. No. 4.5e-209;
Mismatches 0;
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                                  100.0%;
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                                                                              397; Conservative
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                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB, AAS07219
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                                  Query Match
Best Local
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                                                                              Matches
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The sequence represents a G protein-coupled receptor-like (GPCR-like) receptor protein. GPCR-like receptors and their associated nucleic acids may be used to identify candidate compounds for their ability to modulate the activity of GPCRs. The sequences therefore are useful for treating and preventing infection by endoparasitic and ectoparasitic invertebrate parasites, especially helminths and insects, and particularly ailments related to aberrant neurological and neuromuscular function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 RYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYPL------YYSQNLKTMVIENV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herblicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 FLINLAVSDLLLCITAVPITPVLAFMKRWIFGIIMCKLVPTCQAFSVLISSWSLCYIAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 TLCGDFCGEFNWQSDEISKLTYTTSLLIQLIIPAIIMSFCYLMILQKVQTDWLVDEGSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 CIQIARAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 CIDVNAIL--QOFNDWIVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLINLIPTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 PYCGHPCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGET----
                                                                                                                                                      Using G-protein-coupled receptor (GPCR)-like receptors to identify candidate compounds for the treatment and prevention of invertebrate parasites, especially helminths and insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 COSLTOKORSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW----
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 LKROPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%; Score 607.5; DB 4; 35.3%; Pred. No. 1.4e-54; ive 76; Mismatches 111;
                                                                        Larsen MJ;
                                                                                                                                                                                                                            Claim 6; Page 110-111; 219pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN23955 standard; protein; 539
                                                                        Kubiak
       99US-0167523P
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                                     (PHAA ) PHARMACIA & UPJOHN
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Best Local Similarity 35.33
Matches 119, Conservative
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                                                                                                        WPI; 2001-343952/36
                                                                        Geary
                                                                                                                        N-PSDB; AAS07208
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       24-NOV-1999;
                                                                        Lowery DE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a G protein-coupled receptor-like (GPCR-like) receptor protein. GPCR-like receptors and their associated nucleic acids may be used to identify candidate compounds for their ability to modulate the activity of GPCRs. The sequences therefore are useful for treating and preventing infection by endoparasitic and ectoparasitic invertebrate parasites, especially helminths and insects, and particularly ailments related to aberrant neurological and neuromuscular function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor-like receptor; GPCR-like receptor; helminth; endoparasite; ectoparasite; invertebrate; insect; neurological disorder; neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
                                                                                                                                                                                                                                                                                                                                                        1 MVSSAATISTISTITTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYGFLFVLGIFGNGGVLMAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD
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                 Using G-protein-coupled receptor (GPCR)-like receptors to identify candidate compounds for the treatment and prevention of invertebrate parasites, especially helminths and insects.
                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                      91.6%; Score 1899; DB 4; Length 433; 100.0%; Pred. No. 1.4e-190; ive 0; Mismatches 0; Indels
                                                                                 Claim 6; Page 179-180; 219pp; English
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                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 364; Conservative
               G-protein-coupled
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                                                                                                                                                                                                                                                      Sequence 433 AA;
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114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDFTKQPVSIRQALAI 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel polypeptides (P1) from Drosophila melanogaster having the biological activity of a peptide receptor. Molecules of the invention are used to find new plant protection compounds or insecticides, or to find genes encoding a polypeptide involved in the structure of functionally similar receptors in insects This sequence represents a Drosophila melanogaster (fruitfly) peptide receptor described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 ATISTISTITTPST-----ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY
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                                                                                                Score 529; DB 4;
Pred, No. 3.1e-46;
                                                                            318 LKROPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRS
                                                                                                                                                                                                                                                                                                                                                                                          D. melanogaster peptide receptor SEQ ID 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 28-30; 128pp; German.
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30.5%; Pre
tive 76;
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Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insecticides.
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                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and sorperty. The plant is a crop plant such as mainze or soybean. The method of producing a transformed plant to auch as mainze or soybean. The method of producing a plant with the cacombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the polynucleotide or polypeptide is useful for improving plant with the conformant DNA construct is useful for improving plant with the conformant DNA construct is useful for improved plant properties. Conformance to herbicides, extreme osmoctic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth rapid and/or content, improved yield by modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved lightin production or improved galactomannan copiection, improved lightin production or improved galactomannan copiection, improved lightin production or improved galactomannan copiection, improved lightin production or improved galactomannan copiection, improved production. The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence cated for this patent did not format from USPTO at sequence at sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant DNA construct comprising a promoter positioned to provid for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 CIQIARAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 KPLHINDPTKOPVSIROALAITFLIMIVSTLINLPYLMSFEHVDGSFYVQPGET----
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                                                                                                                                                                                                                                                                                                                                                                         Hinkle GJ, Slater SC,
                                                                                                                                                                               21-FEB-2002; 2002US-0360039P.
                                                                                                                                   20-FEB-2003; 2003US-00369493
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Matches 119; Conservative
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SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                       GOLDMAN B S.
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                                       US2003233675-A1
                                                                                    18-DEC-2003
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                                                                   301 YVWISVKIN----QRARAKPGSKSSRRERADRDRKKRTNRMLIAMVAVPGLSWLPINVV 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating call signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                             ----ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC
                                                     YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL
                                                                                                          NLVKOF-KKEPEWLKROPPFWAINAHVIAMSLVVWNPLLPFWLT---RKOKRSGL----
                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 41472; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.5%; Score 529; DB 4; Length 60 Best Local Similarity 30.5%; Pred. No. 3.8e-46; Matches 136; Conservative 76; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 41472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EW;
                                                                                                                                                                --SKILNSTEGSKKAGGSGLRGIQLH 380
                                                                                                                                                                                          414 SNNNIINITRGYNRSDRNTC-GPRLH 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers
                                                                                                                                                                                                                                                             ABB71560 standard; protein; 600 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical
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202
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human immunodeficiency virus; HIV; cancer; Parkinson's disease; diabetes; obesity; atherosclerosis; thrombosis; stroke; renal failure; inflammation; rheumatoid arthritis; autoimmune disorder; neurological disorder; schizophrenia; manic depression; dementia; severe mental retardation; dyskinesia; Huntington's disease;
                                                                                                                                                                                                                                                                                                          301 YVWISVKIN----QRARAKPGSKSSRREBADRDRKKRTNRMIJAMVAVFGLSWLPINVV 355
                                                                                                                                                                                                                                                                                      YPKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
                                                                                                                                                                                                                                                                                                                                                                                   New Drosophila melanogaster GPCR nucleic acids and polypeptide useful for inducing an immune response, for identifying homologs and for treating e.g. diabetes, obesity and manic depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents a fruit fly G protein coupled receptor, DmGPCR1.
                    114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI
                                                                                           122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRWKLSTCIGI
                                                                                                                                                                                                                  ----ETPYCGHFCDEANWOSENSRKIYGTTVMLLQFVVPMAVITYC
                                                                                                                                                                                                                                                  242 ISATQAYMQVMTAGSTGPEMPYVRVYČEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIČ
54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP
                                                                                                                                          182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS
                                                                                                                                                                                                                                                                                                                                                             NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT----RKOKRSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fruit fly; G protein coupled receptor; DmGPCR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fruit fly G protein coupled receptor, DmGPCR1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNNNIINITRGYNRSDRNTC-GPRLH
                                                                                                                                                                                                                                                                                                                                                                                                                                    --SKILNSTEGSKKAGGSGLRGIQLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-2000; 2000WO-US029002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith VG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-316333/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tourette's syndrome
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12;

Gaps

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---ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY

6 ATISTISTTTPST-

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or abrogating insect or nematode

New polypeptide, useful for preventing infestation of a plant. Claim 1; Page 239-242; 368pp; English

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Griswold

Kamdar K, Stam L, Valentine S,

Spana B,

WPI; 2003-533019/50.

N-PSDB; AAD57459

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(SYGN) SYNGENTA PARTICIPATIONS

18-DEC-2002; 2002WO-US040525 18-DEC-2001; 2001US-0341512P

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a mammal. The nucleic acids are useful for identifying an animal homolog of DmGPCR, by screening databases or libraries. The compounds identified as binding partners or modulators of GPCR binding are useful for treating diseases in animals, and for control insects that are harmful or cause injury to plants or animals. Diseases treated include infections (e.g. viral and human immunodeficiency virus, HVI), cancer, pain, Parkinson's disease, hypotension, hypertension, diabetes, obesity, atherosclerosis, autoimmune disorders, and psychotic and neurological disorders (axiety, schizophrenia, manic depression, delixium, dementia, severe mental retardation, dyskinesias, Huntington's disease or Tourette's syndrome). The nucleic acids can be used for genetic mapping, and producing the GPCRs. Anti-GPCR antibodies can be used in therapy, diagnostic assays and for modulating GPCR activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WYAMIKDWAPGSVMCHLVPLSNSCSVPVTSWSLTAISLDKFLHINDPTKOPVSIRQALAI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204
                                                                                                                                                                                                                                                                                                                                                               are useful for inducing an immune response against itself
                                                                                                                                                                                                                                                                                                                                                                                                                        6 ATISTISTITIPST-----ISNVITSHSNNGSCIQIABAIAAQGID---DITVDFY
                                                                                                                                                                                                                                                                                                                                                                                                         IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFLINIVSTLINLPYLMSFE--------HVDGSFYVQPG-----
                                                                                                                                                                                                                                                                                                             Gaps
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infestation; insecticide; nematocide; receptor.
                                                                                                                                                                                                                                                                                                              80;
                                                                                                                                                                                                                                                                              25.5%; Score 529; DB 4; Length 600; 30.5%; Pred. No. 3.8e-46; ive 76; Mismatches 154; Indels
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                                                                                                                                                                                                                                                                                                                Conservative
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Matches 136; Conserv
                                                                                                                                                                                                                                                    Sequence 600 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                  The invention relates to a novel G protein-coupled receptor (GPCR) polypeptide and its polynucleotide. The polypeptide is useful for preventing or abrogating insect or nematode infestation of a plant. GPCR polypeptide is useful in cell therapy. The present sequence is fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ATISTISTITIPST-----ISNVITSHSNNGSCIQIAEALAAQGID---DITVDFY
                                                                                                                                                                                                                                                                                                                                   54 IRSIFTFLYGFLFVLGIFGNGGVLMAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP
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                                                                                                                                                                                                                                                                             Length 600;
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20-OCT-2000; 2000US-00693746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMITH V G.
KUBIAK T M.
LARSEN M J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADR03091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-2004
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                                                                                                                                                                  306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR03092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (/LIMS
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ADR03092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method of identifying a modulator of binding and/or function between a Drosophila melanogaster G protein coupled creeptor (DmoDRAI) and a DmoDRAI binding partner, comprising contacting DmoGPCR and the binding partner in the presence of a candidate compound and determining the effect of the compound on binding and/or function. Also described are: a method for controlling a population of insects; and a method of treating or preventing a disease or condition caused by an ectoparasite. The invention is used to control insects, particularly flies, tick, fleas, lice, mites or cockroaches and to prevent or treat a fisease caused by an ectoparasite, particularly Alzheimer's, parkinson's, Huntington's disease and other neuromuscular and neurodegenerative diseases. This is the amino acid sequence of Drosophila melanogaster G protein coupled receptor 1 (DmGPCR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a modulator of binding and/or function between a Drosophila melanogaster G protein coupled receptor and it's binding partner is useful to control insect populations and prevent or treat disease due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 TFLIMIVSTLINLPYLMSFE--------HVDGSFYVQPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
G protein coupled receptor; DmGPCR1; DmGPCR1 binding partner; insect population control; ectoparasite; Alzheimer's disease; Parkinson's disease; huntington's disease; neuromuscular disease; neurodegenerative disease; fruit fly; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larsen MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 2; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kubiak TM,
                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1999; 99US-00425676.
20-OCT-2000; 2000US-00693746.
06-AUG-2002; 2002US-00213821.
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Matches 136; Conservative
                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith VG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMITH V G.
KUBIAK T M.
LARSEN M J.
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                                                                                                                                                                                                                       US2003162223-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADL83601
                                                                                                                                                                                                                                                                                      28-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
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   NAMES OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET 
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301 YVWISVKIN-----QRARAKPGSKSSRREEADRDRKKKTNRMLIAMVAVFGLSWLPINVV 355
                                                                                                                                                                                                    |: || || || || || || 356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a nucleic acid molecule encoding Drosophila melanogaster G-protein coupled receptor, having fully defined sequence (SI) of 1803, 1443, 1376, 1559, 1568, 1484, 1556, 1569, 1451, 1754 or 1452 nucleotides as given in specification, a sequence that encodes protein having fully defined sequence (S2) of 600, 357, 458, 519, 522, 518, 542, 483, 584 or 483 amino acide as given in specification, or a sequence complementary to (SI). Also described are: an expression vector (II) comprising (I); a host cell (III) transformed with (II); an isolated polypeptide (IV) encoded by (I); an isolated antibody (V) binding to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule encoding Drosophila melanogaster G-protein coupled receptor (DmGPCR), useful in screening DmGPCR modulators for treating disorders e.g. artherosclerosis, myocardial infarction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastrointestinal; atipsoriatic; antiarthritic; antirheumatic; antithyroid; immunosuppressive; cardiant; cerebroprotective; vasotropic; nephrotropic; cytostatic; insecticide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oxidative stress-related neurodegenerative disorder; fruit fly; DmGPCR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiasthmatic; antiarteriosclerotic; neuroprotective; antiinflammatory;
                                                                                                                               NLVKDF-KKEPEWLKROPFFWAINAHVIAMSLVVWNPLLFFWLT---RKOKRSGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-protein coupled receptor; cancer; tumour growth; asthma; psoriasis; inflammatory bowel disease; multiple sclerosis; thyroiditis; rheumatoid arthritis; metabolic disorder; artherosclerosis; autoimmune disorder; organ transplantation; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila G-protein coupled receptor DmGPCR1.
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                                                                                                                                                                                                                                                                                                                               357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                                                                                                                                                                                                                                                                                                                                                                                                    1 | : | : | : | : | | | 414 SNNNIINITRGYNRSDRNTC-GPRLH 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            renal failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 29; SEQ ID NO 2; 101pp; English.
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composition (VII) comprising (II), (II), (IV) or (V) and a carrier or composition (VII) comprising (I), (II), (IV) or (V) and a carrier or diluent. (I) is useful for identifying a compound which binds (I) and indentifying an animal homologue of (I). (II) is useful in producing (IV) or a homologue or their fragment. (IV) is useful for inducing an immune componee in a memmal against (IV) and in identifying a compound binding to (IV). (IV) is useful in identifying a compound binding to (IV). (IV) is useful in identifying a compound that modulates the activity of (IV) and in identifying a modulator of binding between (IV) and a DmGPCR binding partner. (I), (IV), (V) or (VI) is useful in treating cancer cell, tumour growth. (I) or (IV) is useful in treating cancer cell, tumour growth. (IV) is useful in treating cancer cells, inflammatory bowel disease, multiple sclerosis, thyroiditis, rheumatoid arthritis. (VI) is useful in treating disease as the condition such as metabolic disorder, interaction, myccardial inflammatory backer, renal failure, oxidative stress-inflamman disorder, organ transplantation, myccardial inflammatory disorder, and cancer. (VI) is useful for relating disease in animals and for control of insect that are injurious or harmful to plants or animals. This is the amino acid sequence of prosophila G-protein coupled receptor DmGPCRI.
                         8888888888888888888888888
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Sequence 600 AA;

12; 356 121 181 204 247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305 5 ANLSWLSTITTISSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQP 301 YVWISVKIN-----QRARAKDGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 6 ATISTISTITIPST-----ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY IRSIPTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 114 WYAMIKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPIKQPVSIRQALAI 122 LYTPMGRWAFGRSLCHLVSFAQGCSIYISTITLITSIAIDRYFVIIYPFHPRMKLSTCIGI -----HVDGSFYVQPG-----182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS -----ETPYCGHPCDEANMQSENSRKIYGTTVMLLQFVVPMAVITYC 306 NLVKDP-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----Gaps 80; Length 600; 25.5%; Score 529; DB 8; Length 600 30.5%; Pred. No. 3.8e-46; ive 76; Mismatches 154; Indels 414 SNNNIINITRGYNRSDRNTC-GPRLH 438 --SKILNSTEGSKKAGGSGLRGIQLH 380 174 TFLIWIVSTLINLPYLMSFE-----136; Conservative Local Similarity 62 54 205 357 Query Match Matches 셤 a È 셤 ò 셤 ઠ 쇰 ò 셤 કે 셤 δ 셤 ò ઠ

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Virucide, Antiinflammatory, Anti-HIV, Antiparkinsonian; Hypotensive, Hypertensive, Antidiabetic, Antirchumatic, Antiarthritic, Anorectic, Antiarterioscieric, Antiarthric, Cerebroprotective, Vasotropic, Immunosuppressive, Analgesic, Cytostatic, Nephrotropic, Neuroleptic,
             Ź
             ADV91972 standard; protein; 600
                                                                            (first entry)
                                                                                                             DmGPCR1, SEQ ID 2.
                                                                              10-MAR-2005
                                             ADV91972;
ADV9197
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The present invention relates to a method (M1) for identifying a modulator of binding between a Drosophila melanogaster G-protein coupled receptor (DMGPCR) and a DMGPCR binding partner. The method involves contacting a DmGPCR binding partner and a composition comprising a DmGPCR in the presence and absence of a putative modulator compound; detecting binding between the binding partner and the DmGPCR and determining compared to binding in absence of the putative modulator is increased or decreased compared to binding in absence of modulator. DmGPCR modulators cidentified by (M1) are useful for treating diseases such as viral infection caused by HIV-1 or HIV-2, pain, cancer, Parkinson's disease, thrombosis, stroke, renal failure, inflammation, rheumatoid arthitis, cutcoimmune disorder or psychotic and neurological disorder. The present sequence is one such DmGPCR. Identifying modulator of Drosophila melanogaster G-protein coupled receptor (DmGPCR) useful for treating diseases such as cancer, obesity, etc., by determining effect of modulator on binding between DmGPCR and Neuroprotective, viral infection, HIV infection; pain; cancer; Parkinsons disease; hypotension; hypertension; diabetes; obesity; atherosclerosis; thrombosis cerebrovascular ischemia; renal failure; inflammation; rheumatoid arthritis; autoimmune disease; psychotic disorder; neurological disease; G-protein coupled receptor; Ξ̈́ Larsen Disclosure; SEQ ID NO 2; 92pp; English Kubiak TM, 20-OCT-2000; 2000US-00693746. 99US-00425676 (PHAA) PHARMACIA & UPJOHN Drosophila melanogaster. DmGPCR binding partner. Smith VG, 2005-077883/09. WPI; 2005-077883/ N-PSDB; ADV91971. 22-OCT-1999; US6835546-B1 Lowery DE,

Gaps 80; 25.5%; Score 529; DB 9; Length 600, 30.5%; Pred. No. 3.8e-46; Live 76; Mismatches 154; Indels Best Local Similarity 30.5 Matches 136, Conservative Sequence 600 AA; Query Match

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242 ISAIQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLGFVLPFPIISIC 300 181 62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121 204 182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVBATLMLNGSFVAQGSGFIBAPDS ---ETPYCGHPCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 114 WYAMTKOWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI -----HVDGSFYVQPG-----ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 6 ATISTISTITIPST-----ISNVITSHSNNGSCIQIARAIAAQGID---DITVDFY 54 IRSIFTFLYGFLFVLGIFGNGGVLMAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 174 TPLIWIVSTLINLPYLMSFE-----205

247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305

-----HVDGSFYVQPG-----

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240 DSTSATQAYMQVMTAGSTGPEMPYVRVYCES-NWPSEQYRKVFGAITTTLQFVLPFFIIS 298
     60 QFVQIRFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPF 119
                                                                                                                                                                                  245 YCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLT 303
                                                                                                                                                                                                   299 ICYVWISVKLN----QRARAKPGSKSSRREBADRDRKKRTNRMLIAMVAVFGLSWLPIN 353
                                                                                                                                                                                                                                   LLNLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT----RKQKRSGL--- 356
                                                                                                                                                                                                                                                   354 VVNIPDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAMLNENFRKEFKHVLPCF 411
                                                                                                         180 GIIVSIWVIALLATVPYGMYMKMTNELVNGTOTGNETLVEATLMLNGSFVAQGSGFIEAP
                              TPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQAL
                                                                                                                                 205 ------ETPYCGHFCDRANWQSENSRKIYGTTVMLLQFVVPMAVIT
                                                                                                                                                                                                                                                                                                      : |: | : | : | | 12 NPSNNNIINITRGYNRSDRNTC-GPRLH 438
                                                                                                                                                                                                                                                                                       ----SKILNSTEGSKKAGGSGLRGIQLH 380
                                                                              172 AITFLIWIVSTLINLPYLMSFE-----
                                                                                                                                                                                                                                                                                                                                                                              AAU03811 standard; protein; 376
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of binding a Drosophila melanogaster G-protein coupled receptor (DmGPCR) with a DmGPCR binding partner. The invention is used to control an insect population, particularly a fly, fruk, mite, flea or cockroach population, or to treat or prevent a disease or condition caused by ectoparasites, particularly in a companion animal, livestock, horse or a human. The present sequence represents the amino acid sequence of a Drosophila melanogaster G-protein
                                                     |: || || || || || 356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binding a Drosophila melanogaster G-protein coupled receptor with a binding partner or modulator is useful to control an insect population or to treat or prevent a disease or condition caused by ectoparasites.
                                                                                                                                                                                                                                                                                fruit fly; G-protein coupled receptor; DmGPCR; insect populatio control;
fly; tick; mite; flea; cockroach; ectoparasite; receptor.
                                     NLVKDF-KKEPEWLKROPFFWAINAHVIAMSLVVWNPLLFFWLT---RKOKRSGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.1%; Score 521; DB 7; Length 60 30.4%; Pred. No. 2.7e-45; ive 76; Mismatches 152; Indels
                                                                                                                                                                                                                                                      Pruit fly G-protein coupled receptor, DmGPCR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Larsen MJ;
                                                                                       357 -- SKILNSTEGSKKAGGSGLRGIQLH 380
                                                                                                       SNNNIINITRGYNRSDRNTC-GPRLH 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2; 53pp; English.
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                                                                                                                                                                              ADE14524 standard; protein; 600
                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-2002; 2002US-00213821
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20-OCT-2000; 2000US-00693746.
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coupled receptor, DmGPCR
                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE, Smith VG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOWERY D E.
SMITH V G.
KUBIAK T M.
LARSEN M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-843918/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADE14523
                                                                                                                                                                                                                                                                                                                                               US2003180297-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 600 AA;
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                                                                                                                                                                                                       ADE14524;
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The sequence represents a G protein-coupled receptor-like (GPCR-like) receptor protein. GPCR-like receptors and their associated nucleic acids may be used to identify candidate compounds for their ability to modulate the activity of GPCRs. The sequences therefore are useful for treating and preventing infection by endoparasitic and ectoparasitic invertebrate parasites, especially helminths and insects, and particularly ailments related to aberrant neurological and neuromuscular function
                                                                              G protein-coupled receptor-like receptor; GPCR-like receptor; helminth; andoparasite; ectoparasite; invertebrate; insect; neurological disorder; neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech; fruitfly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Using G-protein-coupled receptor (GPCR)-like receptors to identify candidate compounds for the treatment and prevention of invertebrate parasites, especially helminths and insects.
G protein-coupled receptor-like (GPCR-like) receptor protein #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Larsen MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 118-119; 219pp; English.
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13

Gaps

84;

21

52 FYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPV 111

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2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAAS--DEXRSGGIIHN 59

6 ATISTISTITIPST-----ISNVITSHSNNGSCIQIAEAIAAQGIDD----ITVD

Matches 136; Conservative

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                                                                                            SLTQKQRSD-----ATSRKKKVNYILLAMVVTFIGCWLPLTLLNLVKDPKKEP 315
                                                                                                                                                                                                                                   89 ARNVFLIALIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
                                                                                                                   ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208
                                                                                                                                                     CCHPCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKV8KDMIIQNAQFCQ 267
                                                                                                                                                                                                EWLKRQPFFWAINAHVIAMSLVVWNPLLP-------FWLTRKOKRSG-LS 357
                                                          Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                29 NNGSCIQIARAIAAQGIDDITVDPYIRSIPTFLYGFLFVLGIFGNGGVLWAVARNKRLQS
                                 Gaps
                                 65;
                Length 376;
                                 Indels
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               ;; Score 515.5; DB 4;
;; Pred. No. 5.3e-45;
78; Mismatches 131;
                                                                                                                                                                                                                                                         358 KILN----STEGSKKAGGSGLRGIQLHDLLP 384
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                                                                                                                                                                                                                                                                                                                                                                      Bacterial polypeptide #6944.
                         Best Local Similarity 30.3%;
Matches 119; Conservative 7
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAO Y.
HINKLE G J.
SLATER S C.
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Sequence 376 AA;
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                  Query Match
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(SLAT/)
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Sequence 374 AA;

267 284 61 VPNLFILSLSCSDIVVCCTSATITPITAFKGGWIFGBALCRIAPFIAGISLCFSTFTLTA 120 EMLKROPFFWAINAHVIAMSLVVWNPLLF-------FWLTRKOKRSG--LS 357 285 ELIKTQEYIFGIATHCIAMTSTVWNFLLYAVLNLQLRAAFIDLMPHMLRRHLNLEGDNSS 344 88 9 268 SLTQKQRSD-----ATSRKKKVNYILLAMVVTFIGCWLPLTLLMLVKDFKKRP 29 NNGSCIQIABALAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS 89 ARNVFLIALIFTDLILVFTALPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 149 ISLDKFLHINDPTKOPVSIROALAITFLIMIVSTLINLPYLMSFEHVDGSFYVQPGETPY CGHPCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYPKILQKVSKOMIIQNAQFCQ Gaps 48; 24.8%; Score 514; DB 8; Length 374; 31.3%; Pred. No. 7.6e-45; 74; Mismatches 128; Indels Matches 114; Conservative Local Similarity KILN 361 209 228 316 358 Query Match

Search completed: May 8, 2006, 09:29:35 Job time : 191 secs

PLLN 348

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8, 2006, 09:34:27; Search time 166 Seconds (without alignments) 999.267 Million cell updates/sec
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cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query
No. Score Match Length DB ID

1 2074 100.0 397 5 U3-10-650-467-105
2 2074 100.0 397 5 U3-10-650-467-105
3 1899 91.6 433 5 U3-10-650-467-107
5 20.3 539 4 U3-10-650-467-107
5 20.3 539 4 U3-10-650-467-107
5 20.3 539 4 U3-10-650-467-107
5 20.3 539 4 U3-10-650-467-107
5 20.3 539 4 U3-10-30-493-608
5 607.5 20.3 539 4 U3-10-30-493-608
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5 607.5 20.3 539 4 U3-10-213-821-2
5 607.5 20.3 550 600 6 U3-11-097-143-4472
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301 PLTLINLVKDFKKEPEWLKROPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRSGLSKIL 360

	RECEPTORS :: US/09/721,870	Length Indels	AOGID 	LILVET	KQPVSIR KQPVSIR	NSRKIYGT NSRKIYGT	KKVNYILIA KKVNYILIA
US-10-369-493-6097 US-10-611-210-11 US-09-799-955-5- US-10-044-592-12 US-10-044-592-74 US-10-225-567A-245 US-10-278-087A-26 US-10-787-098-8 US-11-054-211-21 US-11-054-211-21 US-11-116-727-46 US-09-955-2 US-09-955-2 US-09-955-2 US-09-955-2 US-09-955-2 US-09-955-2 US-09-955-2 US-10-369-493-6183 US-10-489-455-68 US-10-787-098-6 US-09-799-955-7 US-10-787-098-6	PROTEIN-COUPLED 0,467 PLICATION NUMBER TE: 2000-11-24	; Score 2074; DB 5; ; Pred. No. 1.9e-174; 0; Mismatches 0;	MVSSAATISTISTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 	LYGFLFVLGI FGNGGVLWAVARNKRLGSARNVFLLNI JFTDLILVFTAI PVTFWYAMTKD 	WARGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 	STLINLPYLMSFEHVDGSFYVQPGEFPYCGHFCDEANMQSENSKLYGTTVMLLQFVVPM 	AVITYCYFKILQKVSKOMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVYTFIGGWL
373 373 370 370 370 370 370 370	Publication No. US20050176069A1 GENERAL INFORMATION: APPLICANT: Lowery, David E. APPLICANT: Lowery, Timothy G. APPLICANT: Kubiak, Teresa M. APPLICANT: Kubiak, Teresa M. APPLICANT: Larsen, Martha J. TITLE OF INVENTION: MODILATORS OF G FILE REFERENCE: 28341/6223 CURRENT APPLICATION NUMBER: US/10/65 CURRENT APPLICATION NUMBER: CURRENT AP PRIOR APPLICATION NUMBER: CURRENT AP PRIOR APPLICATION NUMBER: CURRENT AP PRIOR FILING DATE: CURRENT FILING DA NUMBER OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF 2.0 ENGTH: 397 LENGTH: 397 TYPE: PRT ORGANISM: Homo sapiens	100.0% 100.0% vative	TISTTTPE	I PGNGGVLV I FGNGGVLV	LVPLSNSCS LVPLSNSCS	MSFEHVDGS MSFEHVDGS	ILOKVSKON LOKVSKON
18.7 18.6 18.6 18.6 18.6 18.6 18.6 18.6 18.4 18.4 18.4 18.3 18.3 18.4 18.3 18.4 18.3 18.4 18.0	ublication No. ÜS200501760 BRRAL INPORMATION: APPLICANT: Gowery, Joavid B APPLICANT: Gowery, Timothy APPLICANT: Kubiak, Teresa APPLICANT: Kubiak, Teresa APPLICANT: Larsen, Martha TITLE OF INVENTION: MODULA, FILE REFERENCE: 28341/6223 CURRENT FILING DATE: 2003 PRIOR FILING DATE: 2003 PRIOR FILING DATE: 2003 PRIOR FILING DATE: 2003 FILOR FILING DATE: 2003 FILOR FILING DATE: 2003 FILOR TO SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 THE SENTENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 TYPE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTION OF SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: 180 SOFTWARE: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQUE SEQ ID NOS: PATENTIAL OR SEQ ID NOS: PATENTIAL OR SEQ ID NOS:	h Similarity 100 97; Conservative	NSSAATIS VSSAATIS	LYGFLFVLGI LYGFLFVLGI	AFGSVMCH AFGSVMCH	TLINLPYL STLINLPYL	VITYCYPK VITYCYPK
28 387.5 29 386.5 31 386.5 32 386.3 34 386.3 35 386.3 36 386.3 36 386.3 37 386.3 38 38.5 40 385.5 41 385.5 44 373.5 44 373.5 45 373.5 45 373.5	Publication No. US20 REMERAL INFORMATION: APPLICANT: Geary, APPLICANT: Geary, APPLICANT: Geary, APPLICANT: Ensen, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TREAT PELLICATION CURRENT FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: NUMBER OF SEQ ID NO SOPTWARE: PATENTION: SEQ ID NO 105 LENGTH: 397 LENGTH: 397 LENGTH: 397 LENGTH: 397 LENGTH: 397 LENGTH: PATENTION ORGANISM: HOMO SAP	atch cal 8	н ч	61 I 61 I	121 P	181 5	241 A
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61 LYGFLFVLGIFGNGGVLMAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTFMYAMTKD 120
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CURRENT APPLICATION NUMBER: US/10/650,467
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 107
                                                                                                                                                                                                                                                                            5; Length 433;
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29.3%; Score 607.5; DB 5; Length 4
Best Local Similarity 35.3%; Pred. No. 6.3e-45;
Matches 119; Conservative 76; Mismatches 111; Indels
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Pred. No. 5.9e-159;
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91.6%; Score 1899; Di
Best Local Similarity 100.0%; Pred. No. 5.99
Matches 364; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo sapiens
US-10-650-467-16
                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-650-467-107
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                                                                                                                                                                     LENGTH: 433
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                                                                                                                                                                                                                                                       APPLICANT: Lowery, David B.
APPLICANT: Geary, Timochy G.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Kubiak, Teresa M.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 28341/6223
CURRENT APPLICATION NUMBER: US/10/650,467
CURRENT FILING DATE: 2003-08-28
PRIOR PPLIATION NUMBER: CURRENT PPLICATION NUMBER: US/09/721,870
PRIOR PPLIATION DATE: CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40
LENGTH: 499
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Publication No. US20050176069A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Geary, David E.
APPLICANT: Geary, Timochy G.
APPLICANT: Larsen, Martha J.
APPLICANT: Mark, Teresa M.
APPLICANT: Larsen, Martha J.
TILLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 28341/6223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 2074; DB 5; Length Best Local Similarity 100.0%; Pred. No. 2.5e-174; Matches 397; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                        Sequence 40, Application US/10550467
Publication No. US20050176069A1
GENERAL INFORMATION:
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US-10-650-467-40
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US-10-650-467-107
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US-10-650-467-40
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APPLICANT: Lowery, David B.
APPLICANT: Comery, David B.
APPLICANT: Geary, Timothy G.
APPLICANT: Kublak, Teresa M.
APPLICANT: Larsen, Martha J.
APPLICANT: Larsen, Martha J.
APPLICANT: Larsen, Martha J.
APPLICANT: Larsen, Martha J.
APPLICANT: David J.
CURRENT APPLICATION NUMBER: US/10/650,467
PRIOR PELICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
PRIOR PILING DATE: CURRENT FILING DATE: 2000-11-24
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APPLICANT: Lowery, David E.
APPLICANT: Simith, Valdin G.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methor TITLE OF INVENTION: Related To The Same
FILE REPERENCE: PHRMO002-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
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                                                                                                                                                                                                                               ; Sequence 8, Application US/09804551B
; Patent No. US20020056151A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Receptors for peptides from insects
; FILE REFERENCE: Le A 34 394
; CURRENT APPLICATION NUMBER: US/09/804,551B
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: DE 100 13 618.4
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 8:
            357 --SKILNSTEGSKKAGGSGLRGIQLH 380
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                                                                                                                                                                                                           US-09-804-551B-8
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TYPE: PRT
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US-10-283-423-2
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Green, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT PELLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PELLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6608
LENGTH: 539
                                                                                                                                                              PLINLIPTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152
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CIDUNAIL--QOPUDWTVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI 65
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Publication No. US20030233675A1
GENERAL INFORMATION:
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APPLICANT: Lowery, David E.
APPLICANT: Smith, Valdin G.
APPLICANT: Smith, Valdin G.
APPLICANT: Smith, Valdin G.
APPLICANT: Smith, Valdin G.
APPLICANT: Marcha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methor
TITLE OF INVENTION: Related To The Same
FILE REFERENCE: 6297.1Cp
CURRENT APPLICATION NUMBER: US/10/736,048
CURRENT PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 168
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
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                                                                                                                                                                                     25.5%; Score 529; DB 4; Length 600; 30.5%; Pred. No. 7.6e-38; ive 76; Mismatches 154; Indels
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PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 185
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 600
                                                                                                                                                                                                                                Matches 136; Conservative
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US-10-736-048-2
                                                                                                                    , ORGANISM: D. melanogaster
US-10-213-821-2
                                                                                                                                                                                                             Similarity
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US-10-736-048-2
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Publication No. US20030180297A1
Publication No. US20030180297A1
Publication No. US20030180297A1
Publication No. US20030180297A1
APPLICANT: Invermition:
APPLICANT: Enwery, David B.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method TITLE OF INVENTION: Related To The Same FILE REFERENCE: 6297.2cp
CURRENT APPLICATION NUMBER: US/10/213,821
PRIOR APPLICATION NUMBER: 09/693,746
PRIOR APPLICATION NUMBER: 09/425,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 TSATQAYMQVMTAGSTGPEMPYVRVYCER-NWPSEQYRKVPGAITTTLQFVLPPFIISIC 300
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25.5%; Score 529; DB 4; Length 600;
Best Local Similarity 30.5%; Pred. No. 7.6e-38;
Matches 136; Conservative 76; Mismatches 154; Indels
                                                                                                                      PRIOR APPLICATION NUMBER: PriorAppNumber: 09/693,746
PRIOR FILING DATE: PriorFilingDate: 2000-10-20
PRIOR APPLICATION NUMBER: PriorAppNumber: 09/425,676
PRIOR PLLING DATE: PriorFilingDate: 1999-10-22
NUMBER OF SEQ ID NOS: 187
SOFTWARE: Patentin version 3.2
LENGTH: 600
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CURRENT FILING DATE: 2002-10-30
Earlier Applications
                                                                                                                                                                                                                                                                                                                  ) ORGANISM: D. melanogaster
US-10-283-423-2
    Application Project
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REPERENCE: CLO00728

CURRENT APPLICATION NUMBER: G6/157, 832

PRIOR PLING DATE: 1999-10-19

PRIOR PLING DATE: 1999-10-19

PRIOR PLING DATE: 1999-10-19

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-11-28

PRIOR PLING DATE: 1999-12-28

PRIOR PLING DATE: 1999-12-28

PRIOR PLING DATE: 1999-12-28

PRIOR PLING DATE: 2000-01-12

PRIOR PLING DATE: 2000-01-12

PRIOR PLING DATE: 2000-01-12

PRIOR PLING DATE: 2000-01-12

PRIOR PLING DATE: 2000-01-12

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                                                                                                                                                                                                                                                                                                                                                        247 YFKILQKVSKDMIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
                                  114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 NLVKOP-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKOKRSGL---- 356
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                                                                                                                                           ----HVDGSFYVQPG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 --SKILNSTEGSKKAGGSGLRGIQLH 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41472, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
                                                                                                                                     174 TFLIWIVSTLINLPYLMSFE-----
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Matches 136; Conservative
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ORGANISM: DROSOPHILA
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Publication No. US20040248791A1

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Syngenta Participations AG
APPLICANT: Spana, Eric
APPLICANT: Stan, Lynn
APPLICANT: Stan, Lynn
APPLICANT: Stan, Lynn
APPLICANT: Griswald, Charles M
ITILE OF INVENTION:
CURRENT PILIOS OF 1034400CT
CURRENT APPLICATION NUMBER: US/10/489,425
CURRENT APPLICATION NUMBER: 06/341,512
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin version 3.1
SEQ ID NO 62
LENGTH: 600
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ANLSWISTITTISSSISTSQLPLVSTINWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61
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                                                                                                      6 ATISTISTITIPST----ISNVITSHSNNGSCIQIARAIAAQGID---DITVDFY
                                                                                                                                        2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQP
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                         Pred. No. 7.6e-38;
; Mismatches 154; Indels
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30.5%; Pre-
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Best Local Similarity 30.5
Matches 136; Conservative
                      Best Local Similarity 30.9
Matches 136; Conservative
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358 KILN----STEGSKKAGGSGLRGIQLHDLLP
316 EWLKROPFFWAINAHVIAMSLVVWNPLLF-
                                                                                                                                                                               ; Sequence 6944, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Caenorhabditis elegans US-10-369-493-6944
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US-10-369-493-6769
US-10-369-493-6769
; Sequence 6769, Application US/103;
; Publication No. US20030233675A1
; GRURRAL INRORMATION:
; APPLICANT: Gao, Yongwei
; APPLICANT: Hinkle, Gregory J.
                                                                                    : | | : : | | : : | | : : 345 PLLNHPTMTITNKPSKQ---
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                                                                                                                                                                  US-10-369-493-6944
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                                                                                                                                                                                  242 TSATQAYMQVMTAGSTGPEMPYVRVYČEB-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300
                                                                                                                                                                                                                   247 YFKILQKVSKDMIIQNAQPCQSLTQKQRSDA-TSRKKKNNYILIAMVVTFIGCWLPLTLL 305
                                                                                                                                                                                                                                       NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL---- 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 ARNVPLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
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---KKQKTDNWEMELSDQQRIAVKRQRTNRMLIGMVVAFACSWIWSVTFNILRDYSYLP. 284
                                 122 LYTFMGRWARGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRWKLSTCIGI 181
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APPLICANT: Geary, Timothy G.
APPLICANT: Mulak, Teresa M.
APPLICANT: Marcha G.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REPREMER: 28341/6223
CURRENT APPLICATION NUMBER: 108/10/650,467
CURRENT PILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
PRIOR PRING DATE: CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 376
TYPE: PRT
                                                                                                                                                                                                                                                                                                         356 NIPDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS
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                 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDFTKQPVSIRQALAI
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                                                                                                                                                                                                                                                                                                                                                       357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                                                                                                                                                                                                                                                                                                                                                                            SUNNI INITEGYNESDENTC-GPRLH 438
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Publication No. US20050176069A1
GENERAL INFORMATION:
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Best Local Similarity 30.3%;
Matches 119; Conservative
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US-10-650-467-22
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Galdrary Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILL OF INVENTION: PLANTS US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
89 ARNVFLLNLIFTDLILVFTAIPVTPMYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 ISLDKFLHINDPTKQPVSIRQALAITFLIMIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfean
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPRENENCE: 38-10($250$2)8
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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APPLICANT: Geary, Timochy G.

APPLICANT: Geary, Timochy G.

APPLICANT: Kubiak, Teresa M.

APPLICANT: Kubiak, Teresa M.

APPLICANT: Larsen, Marcha G.

FILE REFERENCE: 28341/6223

CURRENT APPLICATION NUMBER: US/10/650,467

CURRENT PILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870

PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870

NUMBER OF SEQ ID NOS: 180

SOFTWARE PATENTING DATE: 2.0

SEQ ID NO 26

LENGTH: 457

TYPE: PRT

CRANISM: Homo sapiens

US-10-650-467-26
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Best Local Similarity 30.8%; Pred. No. 3.8e-34;
Matches 117; Conservative 69; Mismatches 117;
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Publication No. US20050176069A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 -----BGSKKAGGSG 373
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58 FTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM 117
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                                                                              29 FITVYLFLFFLGLFGUFGUVTLIYVTCSHKALLSVQNIFILNLAASDCMACILSLPITFITINV
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query	Query Match Length	DB	OI	Description
п	348.5	16.8	384	6	US-10-987-856-15	Sequence 15, Appl
7	346.5	16.7	384	11	US-11-080-991-26	•
m	346.5	16.7	384	11	US-11-183-615-4	4
4	324	15.6	381	σ	US-10-987-856-16	
ß	314	15.1	375	6	US-10-987-856-17	Sequence 17, Appl
ø	304	14.7	420	0	US-10-992-577-6	. A
7	304	14.7	522	σ	US-10-510-018-2	~
80	286.5	13.8	254	σ	US-10-055-877-248	2
Q	286.5	13.8	254	0	US-10-055-877-327	
10	286.5	13.8	254	σ	US-10-055-877-340	340
11	286.5	13.8	254	σ	US-10-877-346-83	
12	285.5	13.8	430	6	US-10-992-577-8	
13	285.5	13.8	430	6	US-10-508-892-2	Sequence 2, Appli
14	285.5	13.8	430	11	US-11-223-294-54	Sequence 54, Appl
15	285.5	13.8	432	σ	US-10-992-577-2	Sequence 2, Appli
16	285.5	13.8	432	11	US-11-223-294-37	
11	284	13.7	417	σ	US-10-992-577-44	~
18	277	13.4	394	1	US-11-183-615-17	
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20	274.5	13.2	389	0	US-10-995-561-837	
21	271.5	13.1	393	10	US-11-304-129-40	

22 267 12.9 393 9 US-10-504-588-8 Sequence 8, Appli 24 266.5 12.9 40 US-11-304-129-48 Sequence 48, Appl 25 262.5 12.7 259 9 US-10-055-877-225 Sequence 225, Appl 26 262.5 12.7 259 9 US-10-055-877-227 Sequence 227, Appl 26 262.5 12.7 259 11 US-11-205-897-29 Sequence 237, Appl 26 262.5 12.7 259 11 US-11-205-897-29 Sequence 27, Appl 27 262.5 12.7 259 11 US-11-205-897-29 Sequence 27, Appl 26 12.6 384 9 US-10-511-294 Sequence 27, Appl 30 261.5 12.6 384 9 US-10-511-294 Sequence 29, Appl 31 261 12.6 384 10 US-11-304-129-49 Sequence 29, Appl 32 261 12.6 384 10 US-11-304-129-49 Sequence 36, Appl 34 260.5 12.6 384 11 US-11-073-420-7 Sequence 77, Appl 35 260.5 12.6 384 11 US-11-073-420-7 Sequence 77, Appl 36 260.5 12.6 384 11 US-11-073-420-4 Sequence 77, Appl 36 257.5 12.4 359 9 US-10-995-561-712 Sequence 712, Appl 36 257.5 12.4 359 9 US-10-995-561-712 Sequence 713, Appl 36 257.5 12.4 389 9 US-10-995-561-712 Sequence 713, Appl 36 257.5 12.4 389 9 US-10-995-561-712 Sequence 713, Appl 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 713, Appl 36 257.5 12.4 389 9 US-10-995-561-712 Sequence 713, Appl 36 257.5 12.4 389 9 US-10-995-561-712 Sequence 713, Appl 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 713, Appl 36 257.5 12.4 384 11 US-11-073-420-8 Sequence 715, Appl 36 257.5 12.4 384 11 US-11-073-420-8 Sequence 715, Appl 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 715, Appl 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 715, Appl 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 715, Appl 36 257.5 12.4 384 11 US-11-073-420-8 Sequence 2, Appli 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 2, Appli 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 2, Appli 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 2, Appli 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 2, Appli 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 2, Appli 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 2, Appli 36 257.5 12.4 389 9 US-10-995-561-713 Sequence 2, Appli 36 257.5 12.4 389 9 US-10-905-561-713 Sequence 2, Appli 36 257.5 12.4 389 9 US-10-905-561-713 Sequence	ALIGNMENTS SESULT 1 19-10-987-856-15 Sequence 15, Application US/10987856 Sequence 15, Application US/10987856 Sequence 15, Application US/10987856 Sequence 15, Application WIS/204 Sequence 15, Application WIS/204 SEQUENCE 15, Application WIS/204 APPLICANT: WEINSHANK, RICHARD L. APPLICANT: WEINSHANK, RICHARD L. APPLICANT: WAINSHANK, RICHARD L. APPLICANT: WAINSHANK, RICHARD L. APPLICANT: WAINSHANK, RICHARD L. APPLICANT: WAINSHANK, RICHARD L. APPLICANT: WAINSHANK, RICHARD L. APPLICANT: WAINSHER, WANY WA APPLICANTION : WODICYING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE YY RECETURE PRIVED THING DATE: 2004-11-12 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR APPLICATION NUMBER: 08/9962,646 PRIOR PILING DATE: 1999-11-25 REGIO NO 15 LENGTH: 384 TYPE: PRT TYPE: PRT ORGANISM: HOMO Sapiens	Query Match 16.8%; Score 348.5; DB 9; Length 384; Best Local Similarity 25.7%; Pred. No. 1.5e-23; Matches 88; Conservative 79; Mismatches 153; Indels 23; Gaps 6; 18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77 18 STLPSQVENHSVHSNFSEKNAQLIAFENDDCHLPLAMIFTLALAYGRVHILGVSGNLALI 62 78 WAVARNKRLQSARNVFLANIFTDLILVFTAIPYTPWYAMTKDMAFGSVMCHLVPLSNSC 137 11
	RESULT US-10- Seque Publ GRNB APP APP APP TIT TIT TIT TIT PRIL PRIL PRIL PRIL PRIL PRIL PRIL PRIL	Que Bess Ocy Db Cy Cy

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Sequence 16, Application US/10987856
Publication No. US20060014242a1
Sequence 16, Application US/10987856
Publication No. US20060014242a1
GENERAL INFORMATION:
APPLICANT: WEINSHANK, RICHARD L.
APPLICANT: WEINSHANK, RICHARD L.
APPLICANT: MEINSHANK, RICHARD L.
APPLICANT: MEINSHANK, RICHARD L.
APPLICANT: MEINSHANK, RICHARD L.
TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, ANI.
TITLE OF INVENTION: MODIFYING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECE.
TITLE OF INVENTION NUMBER: US/10/987, 856
CURRENT FILING DATE: 2004-11-12
PRIOR PHILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/200,673
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                                                                                                            APPLICANT: Tran, Jennifer W.
APPLICANT: Zheng, Xiaozhang W.
APPLICANT: Zheng, Xiaozhang W.
APPLICANT: Lann, Jennifer W.
APPLICANT: Bliott, Richard L.
APPLICANT: Hammond, Marlys L.
TITLE OF INVENTION: SPIRO[ISOBENZOFURAN-1,4'-PIPERIDIN]-3-ONES AND
TITLE OF INVENTION: 3H-SPIROISOBENZOFURAN-1,4'-PIPERIDINS
FILE REFERENCE: U 0.145.39-7;
CURRENT APPLICATION NUMBER: US/11/183,615
CURRENT PILING DATE: 2003-04-09
FRIOR APPLICATION NUMBER: 10/013,846
FRIOR APPLICATION NUMBER: 10/013,846
FRIOR APPLICATION NUMBER: 60/254,990
FRIOR APPLICATION NUMBER: 60/254,990
FRIOR PILING DATE: 2000-12-12
FRIOR PILING DATE: 2000-12-12
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                           Darrow, James W.
De Lombaert, Stephane
Hutchinson, Alan W.
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ORGANISM: homo sapiens
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TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST

TITLE OF INVENTION: ADD OVARIAN CANCER

TITLE OF INVENTION: AND OVARIAN CANCER

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                                                                                                                                                                                                251 LOKVSKOMIIQNAQPCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKD 310
                                                                                                                                                                                                                                     235 YIRLKR----RNNAMDKARDNKYRSSET---KRINIMLLSIVVAFAVCWLPLTIFNTVFD 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 SFEHVDGSFYVQPGBTPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 SITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDE 182
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                                                                                                        183 PPQNVTLDAYKDK-----YVCPD-QPPSDSHRLSYTTLLLLVLQYFGPLCFIFICYFKI
                                                            SPEHVDGSFYVQPGETPYCGHPCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 WHQIIATCHHNLFFLL-CHLTAMISTCVNPIFYGFLNKNPQR 329
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                                                                                                                                                                                                                                                                                                                             311 PKKEPEWLKROPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKR 353
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Publication No. US20060040964A1
GENERAL INFORMATION:
APPLICANT: Bakthavatchalam, Rajagopal
APPLICANT: Blum, Charles A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.7%
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-11-080-991-26
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Sequence 6, Application US/10992577

Sequence 6, Application US/10992577

Publication No. US20050260687A1

GENERAL INFORMATION:

APPLICANT: Gerald, Christophe P.G.

APPLICANT: Jones, Kenneth A.

APPLICANT: Bonini, James A.

APPLICANT: Bonini, James A.

APPLICANT: Bonini, James A.

APPLICANT: Bonini, James A.

APPLICANT: Craig, Douglas A.

TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) RITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) RITLE OF INVENTION: DNA USes Thereof

FILE REFERENCE: 57155-D/JPW

CURRENT APPLICATION NUMBER: US/09/538,036

PRIOR FILING DATE: 1999-09-24

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                                                                                                                                                   62 YGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDW 121
                                                                                                                                                                                                                                                                                                                                                                300 LPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKI 359
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                                                                                                                                                                                                                                                                                                                122 AFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIMIVS 181
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                                                                                                                                                                                                        48 YSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 TLINLPYLMS--FEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 MAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKVNYILIAMVVTFIGCW
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                                                                     Indels
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                 ::<u>-</u>-
                                                                 88; Conservative
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                          Best Local Similarity
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Publication No. US20060014242A1

GENERAL INFORMATION:

APPLICANT: GERALD, CRISTOPHE P.G.

APPLICANT: WALKER, MARY W

APPLICANT: WALKER, MARY W

APPLICANT: WALKER, THEREA

ITILE OF INVENTION: ENCOING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEF

CURRENT FILING DATE: 1795/46166E2A

CURRENT APPLICATION NUMBER: US/10/997,856

CURRENT FILING DATE: 2004-11-22

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PRIOR FILING DATE: 1995-12-01

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPLSNSCSVFVTSWSLTAISLDXFLHINDPTKQPVSIRQALAITFLIMIVSTLINLPYLM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 SFEH----VDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGT----TVMLLQFVVPMAV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 ITYCYFKILQKVSKOMI--IQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 ISPSYTRIWSKLKONHVSPGAANDHYHQ------RRQKTTKMLVCVVVVFAVSWL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 324; DB 9; Length 38; Pred. No. 2.3e-21; 67; Mismatches 139; Indels
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 08/566,096
PRIOR FILING DATE: 1995-12-01
PRIOR APPLICATION NUMBER: 08/349,025
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 381
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| Similarity 25.5%;
| 91; Conservative 6
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ORGANISM: Homo Sapiens
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Best Local Similarity
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LENGTH: 375
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APPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REPRENCE: 21402-231
CURRENT APPLICATION NUMBER: 00/262,892
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR PLILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR PLILING DATE: 2001-01-23
PRIOR PLILING DATE: 2001-01-23
PRIOR PLILING DATE: 2001-01-25
PRIOR PLILING DATE: 2001-01-25
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PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-03-04
PRIOR PLILING DATE: 2001-03-04
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PRIOR PLILING DATE: 2001-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baumgartner, Jason
Shimkets, Richard
Gusev, Vladimir
Vernet, Corine
Taupier Jr., Raymond
Pena, Carol
                                                                               Padigaru, Muralidhara
Miller, Charles
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Burgess, Cahterine
Eisen, Andrew
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                                                                                                                                                                                                                                                   Anderson, David
Ballinger, Robert
Gerlach, Valerie
Spytek, Kimberly
                                                                                                                                                                        Tchernev, Velizar
Zhong, Mei
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 248
LENGTH: 254
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Andrew, David
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Kekuda, Ramesh
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| Sequence 2, Application US/10510018
| Publication No. US20050244896A1
| GENERAL INPORMATION:
| APPLICANT: GOAL'S Sefan
| APPLICANT: Bruggemeier, Ulf
| APPLICANT: Weingarten, Bernhard
| TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
| TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
| TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
| TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
| TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
| TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
| TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
| TITLE OF INVENTION: DATE: 2004-10-01
| PRIOR FILING DATE: 2003-03-21
| PRIOR FILING DATE: 2003-04-02
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: PALENTIN VERSION 3.3
| SEQ ID NO 2
| LEAST SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:|: :|: :| : : || || || || :: |: : |: : || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: 
                                                                                                                                                                                                                                                                      280 RKKKVNYILIAMVVTFIGCMLPLTLLINLVKDFKK-EPEWLKRQPFFWAINAHVIAMSLVV 338
                                                                                                                                                                                                                                                                                                                               50 VDFY----IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLIL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 VPTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQP 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 VSIRQALAITFLIMIVSTLINLPYLMSFEHVDGSFY-----VQPGETPYCGHFCDEANWQ 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 RKKKVNYILIAMVVTPIGCWLPLTLLNLVKDFKK-EPEWLKRQPFFWAINAHVIAMSLVV 338
                                                                                    SENSRKIYGTTVMLLQFVVPMAVITYCYPKILQKVSKDMIIQNAQPCQSLTQKQRSDATS 279
                                                                                                                                                                             212 NOEMRKIYTTVLFANIYLAPLSLIVIMYGRIGISLFRAAVPHTGR----KNOEOMHVVSR 267
155 LTIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYRVRLNSQNKTSPV--YWCRE-DWP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.7%; Score 30%; 2.2.16.19; 25.7%; Pred. No. 2.16.19; tive 73; Mismatches 143; Indels 18; Gaps tive 73; Mismatches 143; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
08-10-055-877-248
'Sequence 248, Application US/10055877
'Fublication No. US20050288241A1
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328 UNPIIYGFFNENFRR 342
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Best Local S:
Matches 81
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OTHER INFORMATION: Description of Artificial Sequence: 7tm 1, 7
OTHER INFORMATION: transmembrane receptor domain consensus sequence US-10-055-877-327
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 327
LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 254;
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Publication No. US20050288241A1
GENERAL INFORMATION:
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spyrek, Kimberly
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Taupier Jr., Raymond
Pena, Carol
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ORGANISM: Artificial Sequence
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Burgess, Cahterine
Bisen, Andrew
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Shimkets, Richard
Gusev, Vladimir
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Zerhusen, Bryan
Andrew, David
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Ratelli, Luca
Kekuda, Ramesh
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APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ference
TITLE OF INVENTION: NOVel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT FILING DATE: 2002-01-22
FRIOR APPLICATION NUMBER: 60/262,892
FRIOR APPLICATION NUMBER: 60/263,598
FRIOR APPLICATION NUMBER: 60/263,799
FRIOR PILING DATE: 2001-01-24
FRIOR PILING DATE: 2001-01-24
FRIOR PILING DATE: 2001-01-25
FRIOR PILING DATE: 2001-01-25
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FRIOR PILING DATE: 2001-01-26
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-03-02
FRIOR FILING DATE: 2001-03-02
FRIOR FILING DATE: 2001-03-02
FRIOR FILING DATE: 2001-03-02
FRIOR FILING DATE: 2001-03-02
                                  132 PLSNSCSVFVTSWSLTAISLDKFLHINDPT--KQPVSIRQALAITFLIWIVSTLINLPYL 189
                                                                       61 GALFVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVLALLLSLPPL 120
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Publication No. US20050288241A1
GENERAL INFORMATION:
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Retelli, Luca
APPLICANT: Retelli, Luca
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Taupier Jr., Raymond
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Baumgartner, Jason
Shimkets, Richard
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Burgess, Cahterine
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Zerhusen, Bryan
Andrew, David
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Bllerman, Karen Grosse, William M Alsobrook II, John P Lepley, Denise M

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APPLICANT
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TITLE OP INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
TITLE OP INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REPRENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT PILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR PILING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-25
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PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-03-02
PRIOR PRIOR APPLICATION NUMBER: 60/275,990
PRIOR PILING DATE: 2001-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 ILQKVSKDMIIQNAQPCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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13.8%; Score 286.5; DB 9; Length 254;
Best Local Similarity 26.9%; Pred. No. 3.3e-18;
Matches 76; Conservative 62; Mismatches 106; Indels 39.
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
APPLICANT: Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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LENGTH: 254
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190 MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFK 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 ILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVYTFIGCWLPLTLLNLVK 309
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APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Radidaru, Muralidhara
APPLICANT: Radidaru, Martin D
APPLICANT: Radidaru, Martin D
APPLICANT: Baytek, Kimberly A
APPLICANT: Baytek, Kimberly A
APPLICANT: Baytek, Kimberly A
APPLICANT: Baytek, Richard A
APPLICANT: Baytek, Martin D
APPLICANT: Baytekets, Richard A
ITILE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REPERBNCE: 21402-124
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR PILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: 7 OTHER INFORMATION: transmembrane receptor Consensus Sequence
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ORGANISM: Artificial Sequence
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RESULT 12 US-10-992-577-8

53;

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131 VPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM 190
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                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 285.5; DB 9; 24.6%; Pred. No. 7.5e-18; vative 81; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
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APPLICANT: HABATA, YUGO
APPLICANT: HABATA, YUGO
APPLICANT: HASOYA, Masaki
APPLICANT: HOSOYA, Masaki
APPLICANT: HOSOYA, Masaki
APPLICANT: HOSOYA, Masaki
TITLE OF INVENTION: Novel RERP-3 And Its DNA
FILE REFERENCE: 2944USOP
CURRENT FILING DATE: 2005-09-09
PRIOR APPLICATION NUMBER: US/11/487,634
PRIOR APPLICATION NUMBER: US/10/487,634
PRIOR APPLICATION NUMBER: OCT/JP02/08466
PRIOR APPLICATION NUMBER: PCT/JP02/08466
PRIOR FILING DATE: 2002-08-22
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 78
SEQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 ----SGLSKILNSTEGSKKAGGSGLRGIQLH 380
CURRENT APPLICATION NUMBER: US/10/508,892
CURRENT FILING DATE: 2004-09-22
PRIOR APPLICATION NUMBER: PCT/EP03/02685
PRIOR PILING DATE: 2003-03-14
PRIOR PILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 5
SEQ IPMARE: Patentin version 3:3
LENGTH: 430
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Publication No. US20060035332A1
GENERAL INFORMATION:
APPLICANT: HINUMA, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.8
Best Local Similarity 24.6
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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US-11-223-294-54
                                                                                                                                                                                                                                                                                                                                                            US-10-508-892-2
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                                                                                                 APPLICANT: Jones, Kenneth A.
APPLICANT: Jones, Kenneth A.
APPLICANT: Bonini, James A.
APPLICANT: Bonini, James A.
APPLICANT: Bonini, James A.
APPLICANT: Bonini, James A.
APPLICANT: Bonini, James A.
APPLICANT: Craig, Douglas A.
TITLE OF INVENTION: And Uses Thereof
FILE REPERENCE: 57155-D/JPW
CURRENT APPLICATION NUMBER: US/10/992,577
CURRENT PILING DATE: 2004-11-18
FRIOR PLING DATE: 2000-03-29
FRIOR PLING DATE: 1995-09-24
FRIOR APPLICATION NUMBER: 09/405,558
FRIOR PLING DATE: 1995-09-24
FRIOR PLING DATE: 1995-09-24
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FRIOR PLING DATE: 1
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Publication No. US20060014218A1
GENERAL INFORMATION:
APPLICANT: Golz, Stefan
APPLICANT: Bruggemeier, Ulf
APPLICANT: Weingartner, Bernhard
TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
FILE REPERENCE: Le A 35 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 FGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHL 130
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Application US/10992577
                                                   GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Jones, Kenneth A.
                           Publication No. US20050260687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-992-577-8
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US-10-508-892-2
   Sequence 8,
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| Sequence 2, Application US/10992577
| Publication No. US20050260687A1
| GENERAL INFORMATION:
| APPLICANT: Gerald, Christophe P.G. |
| APPLICANT: Bonini, James A. |
| APPLICANT: Bonini, James A. |
| APPLICANT: Bonini, James A. |
| APPLICANT: Bonini, James A. |
| APPLICANT: Craig, Douglas A. |
| TITLE OF INVENTION: DAN Encoding Mammalian Neuropeptide FF (NPFF) Receptors |
| TITLE OF INVENTION: DAN Encoding Mammalian Neuropeptide FF (NPFF) Receptors |
| TITLE OF INVENTION NUMBER: US/09/538,036 |
| FILE REFERENCE: 57155-D/JPM |
| CURRENT PELICATION NUMBER: US/09/538,036 |
| PRIOR FILING DATE: 1999-09-24 |
| PRIOR FILING DATE: 1999-09-24 |
| PRIOR FILING DATE: 1999-09-24 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPLTLLNLVXDFKK--BPB----WLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
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                                                                    53; Gaps
Length 430;
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Query Match
13.8%; Score 285.5; DB 11; Length
Best Local Similarity 24.6%; Pred. No. 7.5e-18;
Matches 96; Conservative 81; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Best Local Similarity
Matches 89; Conserv
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                                                                                                                                       298 CWIPLTLINLVKOFKKEPEWLKROPFFWAINAH---VIAMSLVVW------NPLLFFW 346
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4: /cgn2_6/ptodata/1/laa/PcTUS_COMB.pep:*
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Description		Sequence 105, App	Sequence 40, Appl	Sequence 107, App	16,	7	Sequence 22, Appl	Sequence 26, Appl	36,	14,	12,	8,	9	Sequence 10, Appl	6	(A	m	٠,	2	ä	Sequence 5, Appli	7	21,	104	Sequence 21, Appl	104	Sequence 2, Appli	'n
SUMMARIES		US-09-721-870-105	US-09-721-870-40	US-09-721-870-107	US-09-721-870-16	US-09-693-746-2	US-09-721-870-22	US-09-721-870-26	US-09-721-870-36	US-09-721-870-14	US-09-721-870-12	US-09-721-870-8	US-09-721-870-6	US-09-721-870-10	US-09-693-746-6	US-08-513-974B-26	US-08-513-974B-323	US-09-172-353-5	US-08-776-971-21	US-08-776-971-104	US-09-799-955-5	US-09-461-436B-26	US-09-576-290-21	US-09-576-290-104	US-09-716-147-21	US-09-716-147-104	US-09-172-353-2	US-09-172-353-3
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    Sequence 105, Application US/09721870

| Sequence 105, Application US/09721870
| Patent No. 6632621
| GENERAL INFORMATION:
| APPLICANT: Lowery, David E.
| APPLICANT: Kubiak, Teresa M.
| APPLICANT: Larsen, Martha J.
| TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS |
| FILE REPERENCE: 28341/6233 |
| CURRENT APPLICATION NUMBER: US/09/721,870 |
| CURRENT APPLICATION NUMBER: 2000-11-24 |
| NUMBER OF SEQ ID NOS: 180 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 105
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CORGANISM: Homo sapiens
US-09-721-870-105
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Best Local Similarity
US-09-721-870-105
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153 KFLHINDFTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGET---- 206
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ORGANISM: Homo sapiens
US-09-721-870-16
; SEQ ID NO 107
; IENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-107
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                                                                                     Sequence 40. Application US/09721870

Patent No. 6632621

Patent No. 6632621

GERERAL INPORMATION:
APPLICANT: Lowery, David E.
APPLICANT: Geary, Timothy G.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 23341/6223,
CURRENT FILING DATE: 2000-11-24

NUMBER OF SEQ ID NOS: 180

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 40

LENGTH: 499
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Patent No. 6632621

GENERAL INFORMATION:

APPLICANT: Lowery, David E.

APPLICANT: Geary, Timothy G.

APPLICANT: APPLICANT: Arresa M.

APPLICANT: Laresh, Martha J.

TITLE OF INVENTION: MODILATORS OF G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 28341/6223

CURRENT APPLICATION NUMBER: US/09/721,870

CURRENT FILING DATE: 200-11-24

NUMBER OF SEQ IB NOS: 180

SOFTWARE: Patentin Ver. 2.0
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361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
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ORGANISM: Homo sapiens
US-09-721-870-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 PLTLIALVKOPKKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                         121 WAPGSVWCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDFTKQPVSIRQALAITFLIWIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSKIYGTTVMLLQFVVPM
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                                                                                                                                                                                                                                                         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD
                                                                                                                                                                                                                                                                                                                                                                                    121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV
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                                                                                                                              1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF
                                                                                                                                                                                             1 MVSSAATISTISTTTPSTISNVITSHSNNGSCIQIARAIAAQGIDDITVDFYIRSIFTF
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Patent No. 6632631

GENERAL INFORMATION:

APPLICANT: LOWERY, David E.

APPLICANT: Carry, Teresa M.

APPLICANT: LARIEN, MARCHA J.

ITLE OF INVENTION MODULATORS OF G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 28341/6223

CURRENT APPLICATION NUMBER: US/09/721,870

CURRENT APPLICATION NUMBER: US/09/721,870

CURRENT APPLICATION NUMBER: 200-11-24

NUMBER OF SEQ ID NOS: 180

SOFTWARE: PATENTIN VET. 2.0

SOFTWARE: PATENTIN VET. 2.0

SOFTWARE: PATENTIN VET. 2.0
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Length 433;
                                                               Indels
Query Match 91.6%; Score 1899; DB 2; L
Best Local Similarity 100.0%; Pred. No. 3.7e-150;
Matches 364; Conservative 0; Mismatches 0;
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---KKQKTDNWEMELSDQQRIAVKRQRTNRMLIGMVVAFACSWIWSVTFNILRDYEYLP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGHFCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQ 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 SLTQKQRSD------ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP
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                                                                                                                                        Sequence 22, Application US/09721870

Patent No. 663261

GENERAL INFORMATION:

APPLICANT: Lowery, David E.

APPLICANT: Lowery, Timothy G.

APPLICANT: Lowery, Timothy G.

APPLICANT: Lates, Martha J.

TITLE OF INVENTION: MODULAFORS OF G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 28341/6223

CURRENT APPLICATION NUMBER: US/09/721,870

CURRENT FILING DATE: 2000-11-24

NUMBER OF SEQ ID NOS: 180

SOFTWARE: Patentin Ver. 2.0
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Fatent No. 6632621
GENERAL INFORMATION:
APPLICANT: Lowery, David B.
APPLICANT: Geary, Timothy G.
APPLICANT: Laren, Martha J.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 28341/6223
CURRENT FALING DATE: 200-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
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         | | | | | : : | | | | 414 SNNNIINITRGYNRSDRNTC-GPRLH 438
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Best Local Similarity 30.3%
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-22
                                                                                                  RESULT 6
US-09-721-870-22
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Patent No. 6835546

Patent No. 6835546

Patent No. 6835546

APPLICANT: Lowery, David E. APPLICANT: Smith, Valdin G. APPLICANT: Smith, Valdin G. APPLICANT: Lowery, Martha J. TITLE OF INVENTION: Related To The Same APPLICANT: Larsen, Martha J. TITLE OF INVENTION: Related To The Same FILE REFERENCE: 6297.1cp

CURRENT APPLICATION NUMBER: US/09/693,746

CURRENT APPLICATION NUMBER: 09/425,676

PRIOR FILING DATE: 1999-10-22

PRIOR FILING DATE: 1999-10-22
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207 PYCGHPCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265
                                                                                                                        235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ATISTISTTTPST----ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ANLSWL&TITITISSSISTSQLPLVSTINWSLTSPGTISAILADVAASDEDRSGGIIHNQF 61
                                                                                                266 CQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW-----
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25.5%; Score 529; DB 2; Length 600;
Best Local Similarity 30.5%; Pred. No. 6.7e-36;
Matches 136; Conservative 76; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                 318 LKROPFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRS 354
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SOFWHARE: Patentin version 3.1
SEQ ID NO.
LENGTH: 600
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US-09-693-746-2
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US-09-693-746-2
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                                                                       -----QSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 TAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVS
                                                     203 PGETPYCGHFCDEANWQSE-NSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQ
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                                                                                                                                                                                          322 PFFWAINAHVIAMSLVVWNPLLFFWLTRKOKRSGLSKILNSTEGSKKAGGSGLRGI 377
                                                                                                                                                                                                            65;
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lowery, David E.
APPLICANT: Geary, Timothy G.
APPLICANT: Geary, Timothy G.
APPLICANT: Mubiak, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 28341/6223
CURRENT PILLORICATION NUMBER: US/09/721,870
CURRENT PILLOR DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 387
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US-09-721-870-12
; Sequence 12, Application US/09721870
                                                                                                                                                                                                                                                                                                           ; Sequence 14, Application US/09721870; Patent No. 6632621; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 SARNVFLINLIFIDLILVFTAIPVTPMYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLT 147
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                                                                                                                                                                            58 FTFLYGFLFVLGIFGNGGVLMAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM 117
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| Sequence 36, Application US/09721870
| Patent No. 6632621
| GENERAL INFORMATION:
| APPLICANT: Lowery, David E. |
| APPLICANT: Choist, Teresa M. |
| APPLICANT: Marcha J. |
| APPLICANT: Larsen, Marcha J. |
| TILLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS |
| PILE REFERENCE: 28341/6223 |
| CURRENT FILING DATE: 2000-11-24 |
| NUMBER OF SEQ ID NOS: 180 |
| SOFTWARE: Patentin Ver. 2.0 |
| LENGTH: 365 |
| LENGTH: 365 |
| TYPE: PRT
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                                                                                                         23.4%; Score 485.5; DB 2; Length 4 30.8%; Pred. No. 2e-32; tive 69; Mismatches 117; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 -----EGSKKAGGSG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 TKIVHDTKHLNGRAKIGGGG 395
                                                                                                                           Best Local Similarity 30.8%
Matches 117; Conservative
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US-09-721-870-36
                     LENGTH: 457
TYPE: PRT
CRGANISM: Homo sapiens
US-09-721-870-26
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US-09-721-870-36
       ID NO 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 WIVSTLINLPYL----MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVML 233
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; Sequence No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, Timothy G.
; APPLICANT: Lowery, Timothy G.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS; FIEL REFERRINCE: 28341/6223
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENTH: 402
APPLICANT: Lowery, David E.
APPLICANT: Geary, Timothy G.
APPLICANT: Rublak, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
FILE REPERBNES: 28341/6233
CURRENT FILING DATE: 2000-11-24
CURRENT FILING DATE: 2000-11-24
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 381
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Matches 108; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                             67 VLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSV 126
                                                                                                                                                    127 MCHLVPLSNSCSVFVTSWSLTAISLDKF-----LHINDPTKQPVSIRQALAITFLI 177
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| Batent No. 6632621
| GENERAL INFORMATION:
| APPLICANT: Lowery, David E. |
| APPLICANT: Lowery, Timothy G. |
| APPLICANT: Lowery, Timothy G. |
| APPLICANT: Larsen, Martha J. |
| TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 2834/6223 |
| CURRENT APPLICATION NUMBER: US/09/721,870 |
| NUMBER OF SEQ ID NOS: 180 |
| SOFTWARE: Patentin Ver. 2.0 |
| SOFTWARE: Patentin Ver. 2.0 |
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S SVSSILNETTPSYQST--CKIKNNPMEME-
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Matches 108; Conservative
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192 PE--HVDGSFYVQ----PGETPYCGHFCDEANMQSENSRKIYGTTVMLLQFVVPMAVITY 245
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                                                                                                      25 TSHSNNGSCIQIAE--AIAAQGIDDITVDFYIRS-----IFTFLYGFLFVLGIFGN
                                                                    26;
                              18.7%; Score 388; DB 2; Length 458;
llarity 27.7%; Pred. No. 2.7e-24;
Conservative 79; Mismatches 157; Indels
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hospya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Pukusumi, Shoji
APPLICANT: Ogi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING BATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING BATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 14-SEP-1995
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                   Best Local Similarity
Matches 112, Conserv
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US-08-513-974B-26
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US-09-693-746-6
                                   Query Match
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Patent No. 683546

GENERAL INFORMATION

APPLICANT: Lowery, David E.

APPLICANT: Smith, Valdin G.

APPLICANT: Smith, Valdin G.

APPLICANT: Marbiak, Teresa M.

APPLICANT: Marbiak, Teresa M.

APPLICANT: Marbiak, Teresa M.

TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method

TITLE OF INVENTION: Related To The Same

FILE REPERENCE: 6297.1cp

CURRENT FILING DATE: 2000-10-20

PRIOR PILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 168

SOUTHARE: Patentin version 3.1

SEQ ID NO 6

LEASTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WIVSTLINLPYL----MSFEHVDGSFYVQPGETPYCGHPCDEANWQSENSRKIYGTTVML 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOPVVPMAVITYCYFKILQKV8KDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKOWAFGSV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 MCHLVPLSN8CSVFVTSWSLTAISLDKP------LHINDPTKQPVSIRQALAITFLI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 SVSSILNETTPSYQST--CKIKNNPMEME------YFRPFFISMYCAVF 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 IFALCWPPFNLLNCLRDLKLD-NFWRGYFSFVFLSVHLMSMTATAWNPLLYAFM 314
                                     60;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 406
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
22.1%; Score 458; DB 2; Length 400
Best Local Similarity 30.5%; Pred. No. 3.5e-30;
Matches 108; Conservative 77; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: D. melanogaster
                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-721-870-10
                    RESULT 13
U8-09-721-870-10
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US-09-693-746-6
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134 SNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFE 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
18.6%; Score 386; DB 2; Length 370;
Best Local Similarity 27.5%; Pred. No. 3.1e-24;
Matches 96; Conservative 83; Mismatches 146; Indels 24; Gaps
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PRILING DATE: 20-JAN-1995
PRIOR APPLICATION NUMBER: 3P 7-007177
PRILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19 6-326611
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19 6-270017
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19 6-236357
PRIOR APPLICATION NUMBER: 19 6-236356
PRIOR APPLICATION NUMBER: 19 6-236356
PRIOR APPLICATION NUMBER: 19 6-189274
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APPLICATION NUMBER: 10 6-189272
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AUGUSTA APPLICATION DATA:
AUGUSTA APPLICATION NUMBER: 10 6-189272
PRIOR APPLICATION NUMBER: 10 6-189272
PRIOR APPLICATION NUMBER: 10 6-189272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFRENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INPORMATION:
TELEPAX: 617-523-3400
INPORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS:
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MOLECULE TYPE: peptide

US-08-513-974B-26
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Search completed: May 8, 2006, 09:35:08 Job time : 49 secs

